

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 13:51:18 ; Search time 4501 Seconds  
(without alignments)  
578.093 Million cell updates/sec

Title: US-10-604-726A-8797

Perfect score: 252  
Sequence: 1 ggggtatctgcaactgagag.....tctctcttgcacaccc 252

Scoring table: IDENTITY NUC

Gap 10.0 , Gapext 1.0

Searched: 15754707 seqs, 5162687648 residues

Total number of hits satisfying chosen parameters: 22946898

Minimum DB seq length: 0

Maximum DB seq length: 120

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 17: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 18: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 19: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 20: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 21: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 22: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	32	12.7	32	11	US-10-536-560-26233
C 2	32	12.7	32	11	US-10-536-560-38260
C 3	32	12.7	32	11	US-10-536-560-175427
C 4	32	12.7	32	11	US-10-536-560-325266
C 5	32	12.7	32	11	US-10-536-560-388542
C 6	32	12.7	32	11	US-10-536-560-390712
C 7	29	11.5	29	11	US-10-536-560-399537
C 8	29	11.5	116	21	US-11-443-428A-328462
C 9	25.4	10.1	64	19	US-11-130-645A-206881
C 10	25.4	10.1	64	19	US-11-130-645A-676631
C 11	25.2	10.0	103	21	US-11-443-428A-567727

C 12	24.8	9.8	113	21	US-11-443-428A-626563
C 13	24.2	9.6	63	19	US-11-130-645A-109784
C 14	24.2	9.6	63	19	US-11-130-645A-445004
C 15	24.2	9.6	63	19	US-11-130-645A-446298
C 16	24.2	9.6	64	19	US-11-130-645A-22287
C 17	24.2	9.6	64	19	US-11-130-645A-169416
C 18	24.2	9.6	64	19	US-11-130-645A-348741
C 19	24.2	9.6	64	19	US-11-130-645A-689158
C 20	23.8	9.4	63	19	US-11-130-645A-498699
C 21	23.8	9.4	64	19	US-11-130-645A-245318
C 22	23.8	9.4	64	19	US-11-130-645A-455660
C 23	23.8	9.4	114	21	US-11-497-489A-250527
C 24	23.8	9.4	115	21	US-11-497-489A-201561
C 25	23.6	9.4	64	19	US-11-130-645A-628544
C 26	23.6	9.4	97	12	US-10-708-951-59270
C 27	23.6	9.4	117	20	US-11-503-243A-338191
C 28	23.4	9.3	100	11	US-10-546-139A-1
C 29	23.4	9.3	106	21	US-11-443-428A-709830
C 30	23.4	9.3	115	21	US-11-443-428A-515014
C 31	23.2	9.2	64	19	US-11-130-645A-524987
C 32	23.2	9.2	64	19	US-11-130-645A-538342
C 33	23.2	9.2	81	11	US-10-536-560-457
C 34	23	9.1	63	19	US-11-130-645A-122147
C 35	23	9.1	64	19	US-11-130-645A-44883
C 36	23	9.1	64	19	US-11-130-645A-132874
C 37	23	9.1	64	19	US-11-130-645A-311109
C 38	23	9.1	64	19	US-11-130-645A-325285
C 39	23	9.1	64	19	US-11-130-645A-415331
C 40	23	9.1	64	19	US-11-130-645A-613037
C 41	23	9.1	64	19	US-11-130-645A-715805
C 42	23	9.1	64	19	US-11-130-645A-726268
C 43	23	9.1	64	19	US-11-130-645A-745478
C 44	23	9.1	65	19	US-11-130-645A-728884
C 45	23	9.1	83	13	US-11-635-706-14106

ALIGNMENTS

RESULT 1  
US-10-536-560-26233/c  
; Sequence 26233, Application US/10536560  
; Publication No. US20060257851A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; TITLE OF INVENTION: GENES AND USES THEREOF  
; FILE REFERENCE: 06087.0300.PCUI3  
; CURRENT APPLICATION NUMBER: US/10/536,560  
; CURRENT FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 424571  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 26233  
; LENGTH: 32  
; TYPE: RNA  
; ORGANISM: Homo Sapiens  
US-10-536-560-26233

Query Match 12.7%; Score 32; DB 11; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 198 CTCTGGCCCCCTTAATGTACTTCGGGCTCGTA 229  
Db 32 CTCTGGCCCCCTTAATGTACTTCGGGCTCGTA 1

RESULT 2  
US-10-536-560-38260/c  
; Sequence 38260, Application US/10536560  
; Publication No. US20060257851A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD

;; TITLE OF INVENTION: BIOINFORMATICALY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
;; TITLE OF INVENTION: GENES AND USES THEREOF  
;; FILE REFERENCE: 06087.0300.PCUS13  
;; CURRENT APPLICATION NUMBER: US/10/536,560  
;; CURRENT FILING DATE: 2005-05-26  
;; NUMBER OF SEQ ID NOS: 424571  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 38260  
;; LENGTH: 32  
;; TYPE: RNA  
;; ORGANISM: Homo Sapiens  
US-10-536-560-38260

Query Match 12.7%; Score 32; DB 11; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 162 GCAGTCGGCAGGAGGGCGGGGAGACGA 193  
Db 32 GCAGTCGGCAGGAGGGCGGGGAGACGA 1

RESULT 3

US-10-536-560-175427/c  
; Sequence 175427, Application US/10536560  
; Publication No. US20060257851A1  
; GENERAL INFORMATION:

;; APPLICANT: ROSETTA GENOMICS LTD  
;; TITLE OF INVENTION: BIOINFORMATICALY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
;; TITLE OF INVENTION: GENES AND USES THEREOF  
;; FILE REFERENCE: 06087.0300.PCUS13  
;; CURRENT APPLICATION NUMBER: US/10/536,560  
;; CURRENT FILING DATE: 2005-05-26  
;; NUMBER OF SEQ ID NOS: 424571  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 175427  
;; LENGTH: 32  
;; TYPE: RNA  
;; ORGANISM: Homo Sapiens  
US-10-536-560-175427

Query Match 12.7%; Score 32; DB 11; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 15 TGAGAGGGCTGTTAAGCGTCCCAAGTTG 46  
Db 32 TGAGAGGGCTGTTAAGCGTCCCAAGTTG 1

RESULT 4

US-10-536-560-325266/c  
; Sequence 325266, Application US/10536560  
; Publication No. US20060257851A1  
; GENERAL INFORMATION:

;; APPLICANT: ROSETTA GENOMICS LTD  
;; TITLE OF INVENTION: BIOINFORMATICALY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
;; TITLE OF INVENTION: GENES AND USES THEREOF  
;; FILE REFERENCE: 06087.0300.PCUS13  
;; CURRENT APPLICATION NUMBER: US/10/536,560  
;; CURRENT FILING DATE: 2005-05-26  
;; NUMBER OF SEQ ID NOS: 424571  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 325266  
;; LENGTH: 32  
;; TYPE: RNA  
;; ORGANISM: Homo Sapiens  
US-10-536-560-325266

Query Match 12.7%; Score 32; DB 11; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 134 CGCCTGAGTTTGAGCCGACAGCTCGCAG 165  
Db 32 CGCCTGAGTTTGAGCCGACAGCTCGCAG 1

RESULT 5

US-10-536-560-388542/c  
; Sequence 388542, Application US/10536560  
; Publication No. US20060257851A1  
; GENERAL INFORMATION:

;; APPLICANT: ROSETTA GENOMICS LTD  
;; TITLE OF INVENTION: BIOINFORMATICALY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
;; TITLE OF INVENTION: GENES AND USES THEREOF  
;; FILE REFERENCE: 06087.0300.PCUS13  
;; CURRENT APPLICATION NUMBER: US/10/536,560  
;; CURRENT FILING DATE: 2005-05-26  
;; NUMBER OF SEQ ID NOS: 424571  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 388542  
;; LENGTH: 32  
;; TYPE: RNA  
;; ORGANISM: Homo Sapiens  
US-10-536-560-388542

Query Match 12.7%; Score 32; DB 11; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 90 CTCCTCTGCCACGGGCTGAGTTCCGGCTCC 121  
Db 32 CTCCTCTGCCACGGGCTGAGTTCCGGCTCC 1

RESULT 6

US-10-536-560-390712/c  
; Sequence 390712, Application US/10536560  
; Publication No. US20060257851A1  
; GENERAL INFORMATION:

;; APPLICANT: ROSETTA GENOMICS LTD  
;; TITLE OF INVENTION: BIOINFORMATICALY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
;; TITLE OF INVENTION: GENES AND USES THEREOF  
;; FILE REFERENCE: 06087.0300.PCUS13  
;; CURRENT APPLICATION NUMBER: US/10/536,560  
;; CURRENT FILING DATE: 2005-05-26  
;; NUMBER OF SEQ ID NOS: 424571  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 390712  
;; LENGTH: 32  
;; TYPE: RNA  
;; ORGANISM: Homo Sapiens  
US-10-536-560-390712

Query Match 12.7%; Score 32; DB 11; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 57 TTGCTCTCTTTTCTGGATGCAGATCCCTCTG 88  
Db 32 TTGCTCTCTTTTCTGGATGCAGATCCCTCTG 1

RESULT 7

US-10-536-560-399537/c  
; Sequence 399537, Application US/10536560  
; Publication No. US20060257851A1  
; GENERAL INFORMATION:

;; APPLICANT: ROSETTA GENOMICS LTD  
;; TITLE OF INVENTION: BIOINFORMATICALY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
;; TITLE OF INVENTION: GENES AND USES THEREOF  
;; FILE REFERENCE: 06087.0300.PCUS13  
;; CURRENT APPLICATION NUMBER: US/10/536,560  
;; CURRENT FILING DATE: 2005-05-26  
;; NUMBER OF SEQ ID NOS: 424571

```
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 399537
; LENGTH: 29
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-536-560-399537

Query Match      11.5%; Score 29; DB 11; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 GGGTGCAGAGTCTCTGACTCCCTCTGCC 100
Db 29 GGGTGCAGAGTCTCTGACTCCCTCTGCC 1

RESULT 8
US-11-443-428A-328462
; Sequence 328462, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanging
; APPLICANT: Danari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 328462
; LENGTH: 116
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-443-428A-328462

Query Match      11.5%; Score 29; DB 21; Length 116;
Best Local Similarity 61.0%; Pred. No. 1.2e+03;
Matches 47; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 168 GGGCAGGAGGGGGGGGAGAGCAGCGGCTCTGGCCCTTAATTGTTACTTCGGGCTCG 227
Db 29 GTGATGGAGAGAGGTGTGGACTTTGGAGACTGGGTCTATTAGGGCACTCGGGTTCC 88

Qy 228 TATTGTTCTCTCTTCG 244
Db 89 TCCTGTGCTCTCTCTCG 105

RESULT 9
US-11-130-645A-206881
; Sequence 206881, Application US/11130645A
; Publication No. US20070050146A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Amir, Avniel
; APPLICANT: Yael, Karov
; APPLICANT: Ranit, Aharonov
; TITLE OF INVENTION: MicroRNAs and Uses Thereof
; CURRENT APPLICATION NUMBER: US/11/130,645A
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: PCT/US05/16986
; PRIOR FILING DATE: 2005-05-14
; PRIOR APPLICATION NUMBER: US 10/709,577
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 10/709,572
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/666,340
; PRIOR FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: US 60/665,094
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/662,742
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US 60/593,329
; PRIOR FILING DATE: 2005-01-06
; PRIOR APPLICATION NUMBER: US 60/593,081
; PRIOR FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: US 60/522,860
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/522,457
; PRIOR FILING DATE: 2004-10-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 676631
; LENGTH: 64
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-130-645A-206881

Query Match      10.1%; Score 25.4; DB 19; Length 64;
Best Local Similarity 47.1%; Pred. No. 9.3e+03;
Matches 24; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

Qy 46 GGAAGGGCGCTTTGCTTCTGTTTCTGATGATGAGTCTCTGACTCCCTC 96
Db 14 GAAUGCGGUCUGUCUAGCAGTCCUCCUAGGUGUGUCUGUCUCCUC 64

RESULT 10
US-11-130-645A-676631
; Sequence 676631, Application US/11130645A
; Publication No. US20070050146A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Amir, Avniel
; APPLICANT: Yael, Karov
; APPLICANT: Ranit, Aharonov
; TITLE OF INVENTION: MicroRNAs and Uses Thereof
; FILE REFERENCE: 06087.0202.CPUS13
; CURRENT APPLICATION NUMBER: US/11/130,645A
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: PCT/US05/16986
; PRIOR FILING DATE: 2005-05-14
; PRIOR APPLICATION NUMBER: US 10/709,577
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 10/709,572
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/666,340
; PRIOR FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: US 60/665,094
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/662,742
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US 60/593,329
; PRIOR FILING DATE: 2005-01-06
; PRIOR APPLICATION NUMBER: US 60/593,081
; PRIOR FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: US 60/522,860
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/522,457
; PRIOR FILING DATE: 2004-10-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 676631
; LENGTH: 64
```





## RESULT 14

US-11-130-645A-445004  
; Sequence 445004, Application US/11130645A  
; Publication No. US20070050146A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Itzhak  
; APPLICANT: Amir, Avniel  
; APPLICANT: Yael, Karov  
; APPLICANT: Ranit, Aharonov  
; TITLE OF INVENTION: MicroRNAs and Uses Thereof  
; FILE REFERENCE: 06087.0202.CPUS13  
; CURRENT APPLICATION NUMBER: US/11/130.645A  
; CURRENT FILING DATE: 2005-05-16  
; PRIOR APPLICATION NUMBER: PCT/US05/16986  
; PRIOR FILING DATE: 2005-05-14  
; PRIOR APPLICATION NUMBER: US 10/709,577  
; PRIOR FILING DATE: 2004-05-14  
; PRIOR APPLICATION NUMBER: US 10/709,572  
; PRIOR FILING DATE: 2004-05-14  
; PRIOR APPLICATION NUMBER: US 60/666,340  
; PRIOR FILING DATE: 2005-03-30  
; PRIOR APPLICATION NUMBER: US 60/665,094  
; PRIOR FILING DATE: 2005-03-25  
; PRIOR APPLICATION NUMBER: US 60/662,742  
; PRIOR FILING DATE: 2005-03-17  
; PRIOR APPLICATION NUMBER: US 60/593,329  
; PRIOR FILING DATE: 2005-01-06  
; PRIOR APPLICATION NUMBER: US 60/593,081  
; PRIOR FILING DATE: 2004-12-08  
; PRIOR APPLICATION NUMBER: US 60/522,860  
; PRIOR FILING DATE: 2004-11-15  
; PRIOR APPLICATION NUMBER: US 60/522,457  
; PRIOR FILING DATE: 2004-10-04  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 760616  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 445004  
; LENGTH: 63  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-130-645A-445004

Query Match 9.6%; Score 24.2; DB 19; Length 63;  
Best Local Similarity 49.1%; Pred. No. 1.9e+04;  
Matches 26; Conservative 9; Mismatches 18; Indels 0; Gaps 0;  
Qy 125 TTCGCGTGTGCGCCCTGAGTTTGAGGCCACAGCTCGCAGTCGGCGGAGGAG 177  
Db 11 UUCUUGGUUCCUGAGGUUUCAGGCACUAAAACUCUAUGUGGGGAAGGGAG 63

## RESULT 15

US-11-130-645A-446298  
; Sequence 446298, Application US/11130645A  
; Publication No. US20070050146A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Itzhak  
; APPLICANT: Amir, Avniel  
; APPLICANT: Yael, Karov  
; APPLICANT: Ranit, Aharonov  
; TITLE OF INVENTION: MicroRNAs and Uses Thereof  
; FILE REFERENCE: 06087.0202.CPUS13  
; CURRENT APPLICATION NUMBER: US/11/130.645A  
; CURRENT FILING DATE: 2005-05-16  
; PRIOR APPLICATION NUMBER: PCT/US05/16986  
; PRIOR FILING DATE: 2005-05-14  
; PRIOR APPLICATION NUMBER: US 10/709,577  
; PRIOR FILING DATE: 2004-05-14  
; PRIOR APPLICATION NUMBER: US 10/709,572  
; PRIOR FILING DATE: 2004-05-14  
; PRIOR APPLICATION NUMBER: US 60/666,340  
; PRIOR FILING DATE: 2005-03-30  
; PRIOR APPLICATION NUMBER: US 60/665,094

; PRIOR FILING DATE: 2005-03-25  
; PRIOR APPLICATION NUMBER: US 60/662,742  
; PRIOR FILING DATE: 2005-03-17  
; PRIOR APPLICATION NUMBER: US 60/593,329  
; PRIOR FILING DATE: 2005-01-06  
; PRIOR APPLICATION NUMBER: US 60/593,081  
; PRIOR FILING DATE: 2004-12-08  
; PRIOR APPLICATION NUMBER: US 60/522,860  
; PRIOR FILING DATE: 2004-11-15  
; PRIOR APPLICATION NUMBER: US 60/522,457  
; PRIOR FILING DATE: 2004-10-04  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 760616  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 446298  
; LENGTH: 63  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-130-645A-446298

Query Match 9.6%; Score 24.2; DB 19; Length 63;  
Best Local Similarity 49.1%; Pred. No. 1.9e+04;  
Matches 26; Conservative 9; Mismatches 18; Indels 0; Gaps 0;  
Qy 125 TTCGCGTGTGCGCCCTGAGTTTGAGGCCACAGCTCGCAGTCGGCGGAGGAG 177  
Db 11 UUCUUGGUUCCUGAGGUUUCAGGCACUAAAACUCUAUGUGGGGAAGGGAG 63

Search completed: June 19, 2007, 15:43:23  
Job time : 4502 secs

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 13:14:19 ; Search time 2229 Seconds  
(without alignments)  
7814.408 Million cell updates/sec

Title: US-10-604-726A-8797

Perfect score: 252

Sequence: 1 ggggtatctgcaactgagag.....tctctcttttgcacacctcc 252

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 4052000

Minimum DB seq length: 0

Maximum DB seq length: 120

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*

- 1: gb\_env:\*
- 2: gb\_pat:\*
- 3: gb\_ph:\*
- 4: gb\_pl:\*
- 5: gb\_pr:\*
- 6: gb\_ro:\*
- 7: gb\_sts:\*
- 8: gb\_sv:\*
- 9: gb\_un:\*
- 10: gb\_vi:\*
- 11: gb\_ov:\*
- 12: gb\_htg:\*
- 13: gb\_in:\*
- 14: gb\_om:\*
- 15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	27.8	11.0	98	5	S69137 Homo sapien
C 2	26.2	10.4	98	5	S89198 Homo sapien
C 3	25.2	10.0	109	7	AB150733 Homo sapi
C 4	24.8	9.8	92	2	AX900201 Sequence
C 5	24.8	9.8	92	2	BD035734 Sequence
C 6	24.8	9.8	92	2	AR735995 Sequence
C 7	24.6	9.8	103	2	CO471292 Sequence
C 8	24.6	9.8	104	2	CQ480460 Sequence
C 9	24.4	9.7	119	5	AY751306 Homo sapi
C 10	24.2	9.6	96	2	AR431314 Sequence
C 11	23.8	9.4	78	2	AR477180 Sequence
C 12	23.8	9.4	78	2	AR606935 Sequence
C 13	23.8	9.4	78	2	AR701924 Sequence
C 14	23.6	9.4	72	2	AX899202 Sequence
C 15	23.6	9.4	72	2	BD034735 Sequence
C 16	23.6	9.4	72	2	AR734996 Sequence
C 17	23.6	9.4	97	2	AX184498 Sequence
C 18	23.4	9.3	100	2	AX989552 Sequence

19	23.4	9.3	100	2	AX996400	Sequence
20	23.4	9.3	100	2	CQ874706	Sequence
C 21	23.2	9.2	59	2	E37929	Remedy for
C 22	23.2	9.2	81	10	AY390010	Hepatitis
C 23	23.2	9.2	101	2	CQ149122	Sequence
C 24	23.2	9.2	101	2	CQ232396	Sequence
C 25	23.2	9.2	101	2	CQ307710	Sequence
C 26	23.2	9.2	101	2	CQ344556	Sequence
C 27	23.2	9.2	111	5	HSA012224	Homo sapi
C 28	23	9.1	51	6	AF094482	Mus muscu
C 29	23	9.1	54	6	AY177451	Mus muscu
C 30	23	9.1	65	2	BD461670	OLIGONUCL
C 31	23	9.1	65	2	CQ531157	Sequence
C 32	23	9.1	81	10	AF040860	Hepatitis
C 33	23	9.1	120	7	BV012636	M6S201 Ru
C 34	22.8	9.0	60	2	BD477333	OLIGONUCL
C 35	22.8	9.0	60	2	CQ546820	Sequence
C 36	22.8	9.0	110	5	HSRETINT11	Human RET p
C 37	22.6	9.0	66	2	CQ630945	Sequence
C 38	22.6	9.0	66	2	AR472008	Sequence
C 39	22.4	8.9	60	6	MUSIGXYZ	Mouse Ig S-
C 40	22.4	8.9	98	6	AF387673	Mesocrice
C 41	22.4	8.9	119	2	AX907922	Sequence
C 42	22.4	8.9	119	2	BD043455	Sequence
C 43	22.4	8.9	119	2	AR743716	Sequence
C 44	22.2	8.8	51	2	CQ007958	Sequence
C 45	22.2	8.8	67	2	AX899414	Sequence

#### ALIGNMENTS

RESULT 1	S69137/c	S69137	Homo sapiens	T-cell receptor alpha-chain (TCR V alpha) mRNA,	98 bp	mRNA	linear	PRI 16-MAR-2001
LOCUS	S69137							
DEFINITION	S69137							
ACCESSION	S69137							
VERSION	S69137.1	GI:545967						
KEYWORDS								
SOURCE	Homo sapiens	(human)						
ORGANISM	Homo sapiens							
REFERENCE								
AUTHORS	Mohapatra,S., Mohapatra,S., Yang,M., Ansari,A.A., Parronchi,P., Maggi,E. and Romagnani,S.							
TITLE	Molecular basis of cross-reactivity among allergen-specific human T cells: T-cell receptor V alpha gene usage and epitope structure							
JOURNAL	Immunology 81 (1), 15-20 (1994)							
PUBMED	7510663							
REMARK	GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 144559] from the original journal article.							
FEATURES								
source	1. 98							
	/organism="Homo sapiens"							
	/mol_type="mRNA"							
	/isolate="grass-sensitive individual VI 24"							
	/db_xref="taxon:9606"							
	/tissue_type="peripheral blood"							
	<1. .>98							
gene	/gene="TCR V alpha"							
	<1. .>98							
CDS	/gene="TCR V alpha"							
	/note="allergen-specific; mismatch(30[D->N]) when compared with sequence in paper"							
	/codon_start=1							
	/product="T-cell receptor alpha-chain"							
	/protein_id="AB30241.2"							
	/db_xref="GI:13366254"							
	/translation="DSATYFCAASTNAGKSTFGSGTTLTKPNIQ"							
ORIGIN								

```

Query Match      11.0%; Score 27.8; DB 5; Length 98;
Best Local Similarity 57.5%; Pred. No. 2e+03;
Matches 50; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 65 GTTTCCTGGATGACAGTCTCTGACTCCCTCTGCGACGGGCTGAGTTTCGGGCTCCAGG 124
DB 93 GATATTGGCTTCACAGTGAGGCTAGTCCCAAGGTTGATTTCCTGCATTGGT 34

QY 125 TTCGGGTGTCGCCCTCGAGGTTTGAGGC 151
DB 33 GGTGCTGCTGCACAGAAGTAGGTGGC 7

RESULT 2
LOCUS S69198/c
DEFINITION Homo sapiens T-cell receptor alpha-chain (TCR V alpha) mRNA,
partial cds.
ACCESSION S69198
VERSION S69198.1 GI:545963
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 98)
AUTHORS Mohapatra,S.S., Mohapatra,S., Yang,M., Ansari,A.A., Parronchi,P.,
Maggi,E. and Romagnani,S.
TITLE Molecular basis of cross-reactivity among allergen-specific human T
cells: T-cell receptor V alpha gene usage and epitope structure
JOURNAL Immunology 81 (1), 15-20 (1994)
PUBMED 7510663
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 144557] from the original journal article.
FEATURES
source
1..98
/organism="Homo sapiens"
/mol_type="mRNA"
/isolate="grass-sensitive individual VI 17"
/db_xref="taxon:9606"
/tissue_type="peripheral blood"
<1..>98
/gene="TCR V alpha"
<1..>98
/gene="TCR V alpha"
/codon_start=1.
/product="T-cell receptor alpha-chain"
/protein_id="AAB30239.2"
/db_xref="GI:13236916"
/translation="DSATYFCAASTTNAGKSTFGGGTTLTVKPNIQ"

ORIGIN
Query Match      10.4%; Score 26.2; DB 5; Length 98;
Best Local Similarity 56.3%; Pred. No. 6.6e+03;
Matches 49; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 65 GTTTCCTGGATGACAGTCTCTGACTCCCTCTGCGACGGGCTGAGTTTCGGGCTCCAGG 124
DB 93 GATATTGGCTTCACAGTGAGGCTAGTCCCAAGGTTGATTTCCTGCATTGGT 34

QY 125 TTCGGGTGTCGCCCTCGAGGTTTGAGGC 151
DB 33 GGTGCTGCTGCACAGAAGTAGGTGGC 7

RESULT 3
LOCUS AB150733
DEFINITION Homo sapiens DNA, STS on chromosome 10, D10S08121, sequence tagged
site.
ACCESSION AB150733

```

```

VERSION AB150733.1 GI:62171551
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Taniya,G., Shinya,M., Imanishi,T., Ikuta,T., Makino,S., Okamoto,K.,
Furugaki,K., Matsumoto,T., Mano,S., Ando,S., Nozaki,Y., Yukawa,W.,
Nakashige,R., Yamaguchi,D., Ishibashi,H., Yonekura,M., Nakami,Y.,
Takayama,S., Endo,T., Saruwatari,T., Yagura,M., Yoshikawa,Y.,
Fujimoto,K., Oka,A., Chiku,S., Linsen,S.E., Giphart,M.J.,
Kuleki,J.K., Fukazawa,T., Hashimoto,H., Kimura,M., Hoshina,Y.,
Suzuki,Y., Hotta,T., Mochida,J., Minezaki,T., Komai,K.,
Shiozawa,S., Taniguchi,A., Yamanaka,H., Kamatani,N., Gojobori,T.,
Bahram,S. and Inoko,H.
TITLE Whole genome association study of rheumatoid arthritis using 27 039
microsatellites
JOURNAL Hum. Mol. Genet. 14 (16), 2305-2321 (2005)
PUBMED 16000323
REFERENCE 2 (bases 1 to 109)
AUTHORS Taniya,G., Makino,S., Fujimoto,K., Oka,A., Hayashi,H., Denda,A.,
Linsen,S.E., Ikuta,T., Shinya,M., Endo,T., Tomizawa,M., Tokubo,E.,
Sato,R., Takaki,A., Nagatsuka,Y., Watanabe,H., Adachi,S.,
Makino,Y., Nakano,S., Yamamoto,A., Yoshida,K., Okamoto,K.,
Yanaguchi,D., Ishibashi,H., Yonekura,M., Takayama,S., Nakami,Y.,
Saruwatari,T., Brand,A., van Hiltten,J.A., van de Watering,L.M.,
Giphart,M.J., Bahram,S., Kulski,Y.J. and Inoko,H.
TITLE Direct Submission
JOURNAL Submitted (12-DEC-2003) Hidetoshi Inoko, Tokai University School of
Medicine, Department of Genetic Information, Boiseidai, Isehara,
Kanagawa 259-1193, Japan (E-mail:hinoko@is.icc.u-tokai.ac.jp,
Tel:81-463-93-1121, Fax:81-463-94-8884)
COMMENT Polymorphisms were confirmed by comparing with the pooled DNA
typing data of 88 Dutch population or 100 Australian. When there
was no significant difference between the Japanese and these
Caucasians, individual typing was performed to confirm
polymorphisms.
FEATURES
Location/Qualifiers
1..109
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="10"
/map="10q23.2"
/note="pooled DNA of 100 Japanese unrelated individuals
sequence tagged site D10S08121"
primer_bind
1..18
/note="5' primer: TCATGACAGGTGGTAGG"
/PCR_conditions="denaturation 96degC 5 min, 57degC 1 min,
72degC 1 min; 40 cycles 96degC 45 sec, 57degC 45 sec,
72degC 1 min"
repeat_region
51..78
/note="sequence tagged site D10S08121"
/rpt_type=tandem
/rpt_unit_seq="cagg"
/complement(89..109)
primer_bind
/note="3' primer: TCAGGAAGTGTCTGTACTCTC"
ORIGIN
Query Match      10.0%; Score 25.2; DB 7; Length 109;
Best Local Similarity 62.9%; Pred. No. 1.4e+04;
Matches 39; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 138 CTGAGTTTTCAGGCGCAGACAGCTCGCAGTCGGGAGGGGGGGGAGAGACGACGG 197
DB 42 CTGAGTTTTCAGGCGCAGGAGGCGAGGCGAGGCTAGCTGACAGAGTACAGCAC 101

QY 198 CT 199
DB 102 CT 103

```

Matches	35;	Conservative	0;	Mismatches	17;	Indels	0;	Gaps	0;
Qy	156	CAGCTCGCAGTTCGGGCGAGGAGCGGGGAGAGACGAGCGGCTCTGGCCCC	207						
Db	13	CAGCTCGAATCGGAGCGGAACAGCGGGCTGGGAGCGCGCGCGCGCCCC	64						
RESULT 6									
AR735995									
LOCUS	AR735995	Sequence 16064 from patent US 6783961.		92 bp	DNA	linear		PAT 11-OCT-2005	
DEFINITION	AR735995	Expressed sequence tags and encoded human proteins							
ACCESSION	AR735995.1	GI:77429735							
VERSION	AR735995.1	GI:77429735							
KEYWORDS	Unknown.								
SOURCE	Unknown.								
ORGANISM	Unclassified.								
REFERENCE	1 (bases 1 to 92)								
AUTHORS	Edwards, J.-B.D.M., Duclert, A. and Giordano, J.-Y.								
TITLE	Expressed sequence tags and encoded human proteins								
JOURNAL	Patent: US 6783961-A 16064 31-AUG-2004;								
	Genset S.A.;								
FEATURES	PRX;	Location/Qualifiers							
source	1..92	/organism="unknown"							
ORIGIN		/mol_type="genomic DNA"							
Query Match		9.8%; Score 24.8; DB 2; Length 92;							
Best Local Similarity		67.3%; Pred. No. 1.8e+04;							
Matches	35; Conservative	0; Mismatches 17; Indels	0; Gaps	0;					
Qy	156	CAGCTCGCAGTTCGGGCGAGGAGCGGGGAGAGACGAGCGGCTCTGGCCCC	207						
Db	13	CAGCTCGAATCGGAGCGGAACAGCGGGCTGGGAGCGCGCGCGCCCC	64						
RESULT 7									
AR735995									
LOCUS	AR735995	Sequence 3158 from Patent WO0160860.		103 bp	DNA	linear		PAT 30-JAN-2004	
DEFINITION	AR735995	Expressed sequence tags and encoded human proteins							
ACCESSION	AR735995.1	GI:41436911							
VERSION	AR735995.1	GI:41436911							
KEYWORDS	Homo sapiens (human)								
SOURCE	Homo sapiens								
ORGANISM	Homo sapiens								
REFERENCE	1	Schlegel, R., Endege, W. O. and Monahan, J. E.							
AUTHORS	Genes differentially expressed in human prostate cancer and their								
TITLE	use								
JOURNAL	Patent: WO 0160860-A 3158 23-AUG-2001;								
	Millennium Predictive Medicine, Inc. (US)								
FEATURES	Location/Qualifiers								
source	1..103	/organism="Homo sapiens"							
		/mol_type="unassigned DNA"							
		/db_xref="taxon:9606"							
ORIGIN									
Query Match		9.8%; Score 24.6; DB 2; Length 103;							
Best Local Similarity		57.0%; Pred. No. 2.1e+04;							
Matches	45; Conservative	0; Mismatches 34; Indels	0; Gaps	0;					
Qy	174	GGAGGGCGGGGAGAGACGAGCGGCTCTGGCCCCCTTAATTGTACTTCGGGCTCGTATTGT	233						
Db	2	GGTACGGGGGAGACGCCGCGCGCTGGAGCGCTGTAGTGGCTTCGCTTCGGTTTTT	61						
Qy	234	CTCTCCTTTTCGCCACCTCT	252						

Db 62 CTCTTCCTTCGCTAACGCC 80

RESULT 8  
CQ480460  
LOCUS CQ480460 104 bp DNA linear PAT 30-JAN-2004  
DEFINITION Sequence 12327 from Patent WO0160860.  
ACCESSION CQ480460  
VERSION CQ480460.1 GI:41446079  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
Catarrhini; Hominidae; Homo.  
1  
Schlegel R., Endege, W.O. and Monahan, J.B.  
Genes differentially expressed in human prostate cancer and their  
use  
Patent: WO 0160860-A 12327 23-AUG-2001;  
Millennium Predictive Medicine, Inc. (US)  
JOURNAL  
FEATURES  
Location/Qualifiers  
1..104  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 9.8%; Score 24.6; DB 2; Length 104;  
Best Local Similarity 57.0%; Pred. No. 2.1e+04;  
Matches 45; Conservative 0; Mismatches 34; Indels 0; Gaps 0;  
Qy 174 GGAGGGCGGGGAGAGAGCGGCTCTGCGCCCTTAATTCGCTTCGGGCTCGTATTGT 233  
Db 2 GGTACGGGGGAGAGAGCGGCGCGCGCTGCGAGCTGTAGTGGCTTCGCTTCGGTTTTT 61  
Qy 234 CTCTCCTTTCGCCACCTCC 252  
Db 62 CTCTTCCTTCGCTAACGCC 80

RESULT 9  
AY751306  
LOCUS AY751306 119 bp mRNA linear PRI 19-MAY-2005  
DEFINITION Homo sapiens clone RW33 T cell receptor beta chain mRNA, partial  
cbs.  
ACCESSION AY751306  
VERSION AY751306.1 GI:54111802  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
Catarrhini; Hominidae; Homo.  
1 (bases 1 to 119)  
Barcy S., Huang M.L., Corey L. and Koelle, D.M.  
Longitudinal Analysis of Herpes Simplex Virus-Specific CD4+ Cell  
Clonotypes in Infected Tissues and Blood  
J. Infect. Dis. 191 (12), 2012-2021 (2005)  
PUBMED 15897986  
REFERENCE 2 (bases 1 to 119)  
Barcy, S.  
Direct Submission  
Submitted (14-SEP-2004) Laboratory Medicine, University of  
Washington, 1959 N.E. Pacific Street, Rosen Bldg, Room 154,  
Seattle, WA 98109, USA  
JOURNAL  
FEATURES  
Location/Qualifiers  
1..119  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="RW33"  
/cell\_type="Herpes simplex virus specific CD4+ T

lymphocyte"  
/tissue\_type="herpetic skin lesion"  
<1..>119  
/codon\_start=1  
/product="T cell receptor beta chain"  
/protein\_id="AAV28660.1"  
/db\_xref="GI:54111803"  
/translation="NVNALLLGDLSALYLCASSSGTTPGYTFTGSGTRLIVVDL"

ORIGIN  
Query Match 9.7%; Score 24.4; DB 5; Length 119;  
Best Local Similarity 54.4%; Pred. No. 2.5e+04;  
Matches 49; Conservative 0; Mismatches 41; Indels 0; Gaps 0;  
Qy 37 CCCCAAGTTGGAAGGGCGCTTTCGCTTCGTTTTCTGGATGAGAGTCTCTGACTCCCTC 96  
Db 9 CGCCTTGTGCTGGGGACTCGGCCCTTTAATCTCTGCGCCAGCAGTTCGGGACACCCCTA 68  
Qy 97 TGCCACGGGCTGAGTTTCCGGCTCCAGGTT 126  
Db 69 TGGCTACACCTTCGGTTCGGGGACCAGGTT 98

RESULT 10  
AR431314  
LOCUS AR431314 96 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 1 from patent US 6651010.  
ACCESSION AR431314  
VERSION AR431314.1 GI:40193289  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 96)  
Han, K., Kim, D. and Kim, H.-J.  
Vector-based method for visualizing secondary structure of RNA  
molecules  
Patent: US 6651010-A 1 18-NOV-2003;  
INHA University Foundation; Incheon-si;  
KRX;  
FEATURES  
Location/Qualifiers  
1..96  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 9.6%; Score 24.2; DB 2; Length 96;  
Best Local Similarity 59.4%; Pred. No. 2.8e+04;  
Matches 41; Conservative 0; Mismatches 28; Indels 0; Gaps 0;  
Qy 32 GCGGTCCCAAGTTGGAAGGGCGCTTTCGCTTCGTTTTCTGGATGAGAGTCTCTGACT 91  
Db 10 GCGGCTCGAGTCGAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 69  
Qy 92 CCCTCTGCC 100  
Db 70 GCTGCTGCC 78

RESULT 11  
AR477180/c  
LOCUS AR477180 78 bp DNA linear PAT 14-MAY-2004  
DEFINITION Sequence 145 from patent US 6696256.  
ACCESSION AR477180  
VERSION AR477180.1 GI:47234454  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 78)  
Li, X.  
Method, array and kit for detecting activated transcription factors  
by hybridization array

```

source      1. .78
/mol_type="genomic DNA"

ORIGIN
Query Match      9.4%; Score 23.8; DB 2; Length 78;
Best Local Similarity 59.6%; Pred. No. 3.7e+04;
Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 109 AGTTTCGGCTCAGGTTCCGGTGTGCGCTCAGGTTTGAAGGCCAGACAGCTCGCAGTCG 168
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 78 AGTTTCAAGTCAGAGGTCAGAGAGCTAGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTCAG 19
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 169 GGCAGG 175
      |||||
Db 18 GTCAGAG 12

RESULT 14
AX899202/c
LOCUS      AX899202              72 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION Sequence 15065 from Patent EP1033401.
ACCESSION  AX899202
VERSION     AX899202.1 GI:40054115
KEYWORDS
SOURCE
ORGANISM    Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.

REFERENCE
1
AUTHORS     Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
TITLE       Expressed sequence tags and encoded human proteins
JOURNAL     Patent: EP 1033401-A 15065 06-SEP-2000;
GENSET      Genset (FR)

FEATURES
source      1. .72
/mol_type="Homo sapiens"
/db_xref="taxon:9606"

ORIGIN
Query Match      9.4%; Score 23.6; DB 2; Length 72;
Best Local Similarity 69.6%; Pred. No. 4.3e+04;
Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 128 GCCTGTCCCTCAGGTTTGAAGGCCAGACAGCTCGCAGTCGGGCAG 173
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 58 GCCTGGGGCCCCGGGATCGAGGCGCATCCAGCACAGAGCGGCCAG 13

RESULT 15
BD034735/c
LOCUS      BD034735              72 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Sequence tag and encoded human protein.
ACCESSION  BD034735
VERSION     BD034735.1 GI:22576477
KEYWORDS    JP 2001269182-A/10981.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 72)
AUTHORS     Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
TITLE       Sequence tag and encoded human protein
JOURNAL     Patent: JP 2001269182-A 10981 02-OCT-2001;
GENSET

COMMENT
OS Homo sapiens (human)
PN JP 2001269182-A/10981
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487

```

PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES  
PI JORDAN  
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC  
C12N5/10,  
PC C12P21/02, C12P21/08, C12Q1/68, G06F17/30, C12N15/00, C12N5/00, PC  
G06F15/40  
CC

FEATURES

source

FH

Key

Location/Qualifiers

1..72

/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 9.4%; Score 23.6; DB 2; Length 72;  
Best Local Similarity 69.6%; Pred. No. 4.3e+04;  
Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
QY 128 GCGTGTGCGCCCTGAGTTTTCAGGCCACAGACAGCTGCGCAGTCGGGCAG 173  
||||| .||||| .||||| .||||| .||||| .||||| .||||| .|||||  
Db 58 GCGTGGGGCCCGGGGATCGAGGGCATCCACACAGAGCGGCCAG 13

Search completed: June 19, 2007, 14:28:18  
Job time : 2233 secs

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 13:10:19 ; Search time 372 Seconds  
(without alignments)  
5020.062 Million cell updates/sec

Title: US-10-604-726A-8797  
Perfect score: 252  
Sequence: 1 999ttatcgcgaactgagag.....tctctcttctgcgaacttc 252

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 6225436

Minimum DB seq length: 0  
Maximum DB seq length: 120

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq\_200701.\*  
1: Geneseqn1980s.\*  
2: Geneseqn1990s.\*  
3: Geneseqn2000s.\*  
4: Geneseqn2001as.\*  
5: Geneseqn2001bs.\*  
6: Geneseqn2002as.\*  
7: Geneseqn2002bs.\*  
8: Geneseqn2003as.\*  
9: Geneseqn2003bs.\*  
10: Geneseqn2003cs.\*  
11: Geneseqn2003ds.\*  
12: Geneseqn2004as.\*  
13: Geneseqn2004bs.\*  
14: Geneseqn2005s.\*  
15: Geneseqn2006s.\*  
16: Geneseqn2007s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25.6	10.2	115	6	ABQ76940 Polylinke
2	25.2	10.0	96	15	AEG19874
3	25.2	10.0	96	15	AEG19878
4	24.8	9.8	92	3	AAC11989
5	24.6	9.8	103	5	ABV03167 Human pro
6	24.6	9.8	104	5	ABV12336 Human pro
7	24.2	9.6	105	4	AH336160 Human col
8	23.8	9.4	78	8	ABT11892
9	23.6	9.4	72	3	AAC10990
10	23.6	9.4	97	4	AAH68919
11	23.4	9.3	100	8	ACD69745 E. coli K
12	23.4	9.3	100	8	ACD76587
13	23.4	9.3	100	13	ADR28210
14	23.4	9.3	100	13	ADR99734
15	23.2	9.2	59	3	AAZ89260
16	23.2	9.2	101	4	AAK44587
17	23.2	9.2	101	4	AAK18659

C 18	23.2	9.2	101	4	ABS44245	Abc44245 Human liv
C 19	23.2	9.2	101	6	ABS18824	Abc18824 Human gen
C 20	23.2	9.2	118	12	ACH88031	Ach88031 Human gen
C 21	23	9.1	65	6	ABN28044	Abn28044 Rat splic
C 22	23	9.1	87	6	ABL75509	Ab175509 Corn tass
C 23	22.8	9.0	60	6	ABN43707	Abn43707 Human spl
C 24	22.8	9.0	88	13	ADQ91596	Adq91596 Template
C 25	22.8	9.0	117	9	ADA73750	Ada73750 Carcinoma
C 26	22.6	9.0	66	13	ABN15693	Abn15693 Human gen
C 27	22.6	9.0	66	13	ACN78783	Acn78783 Human GDM
C 28	22.4	8.9	119	3	AAL19710	Aal19710 Human sec
C 29	22.2	8.8	51	4	AAL33390	Aal33390 Human SNP
C 30	22.2	8.8	67	3	AAC11202	Aac11202 Human sec
C 31	22.2	8.8	88	13	ADR50936	Adr50936 Human mus
C 32	22.2	8.8	88	13	ADR50937	Adr50937 Human mus
C 33	22.2	8.8	88	13	ADR50938	Adr50938 Human mus
C 34	22.2	8.8	102	3	AZ60564	Aaz60564 A neublas
C 35	22.2	8.8	102	6	ABT11892	Abt11892 PCR produ
C 36	22.2	8.8	106	2	AAV46418	Aav46418 Ribosomal
C 37	22.2	8.8	115	3	ACL25369	Acl25369 DNA clone
C 38	22.2	8.8	115	9	ACL25369	Acl25369 DNA clone
C 39	22	8.7	68	15	AEE99649	Aee99649 Mouse mir
C 40	22	8.7	89	14	ADX04314	Adx04314 Mouse pri
C 41	22	8.7	93	2	AQ97727	Aaq97727 Toxoplasm
C 42	22	8.7	102	14	AEB50490	Aeb50490 Human myo
C 43	22	8.7	113	4	ABA36569	Ab36569 Probe #15
C 44	21.8	8.7	61	3	AAZ89261	Aaz89261 Human emb
C 45	21.8	8.7	93	14	ACL68051	Acl68051 M. xanthu

# ALIGNMENTS

## RESULT 1

ABQ76940

ID ABQ76940 standard; DNA; 115 BP.

XX

AC ABQ76940;

XX

DT 27-MAR-2003 (first entry)

XX

DE Polylinker ScaI-Li-(BsgI-ScaI) DNA.

XX

Murine; T cell receptor; TCR; hdm2; T cell response; alpha TCR; beta TCR;

antigen-recognising sequence; ARS; fusion construct; cytostatic;

apoptotic; tumour; leukaemia; immunisation; ds.

XX

OS Synthetic.

XX

FN DE10109854-A1.

XX

PD 12-SEP-2002.

XX

PF 01-MAR-2001; 2001DE-01009854.

XX

PR 01-MAR-2001; 2001DE-01009854.

XX

PA ABQ76940 Polylinke

XX

PI Aeg19874 Temp- DNA

XX

PT Aac11989 Human sec

XX

DR Abv03167 Human pro

XX

DR Abv12336 Human pro

XX

DR Aah336160 Human col

XX

XX Abt11892 Transcrip

XX

PT Aac10990 Human sec

XX

PT Aah68919 Human cer

XX

PT Acd69745 E. coli K

XX

New polypeptide of a murine alpha/beta T-cell receptor, useful for treating tumors and leukemia, induces specific lysis or apoptosis of cells expressing hdm2 protein.

Example 2; Fig 6; 52pp; German.

This invention describes a novel murine alphabeta T-cell receptor (TCR) that mediates a hdm2 protein-specific T cell response, a fusion protein (FP) that includes the TCR and nucleic acid encoding it, alpha or beta-



chains of a TCR that include the antigen-recognizing sequence (ARS) of an antibody specific for aa 81-88 of hdm2 (or its complex with HLA-A2-specific antibody) and a method for identifying hdm2-specific antigens. The TCR of the invention has cytostatic and apoptotic activity. The products of the invention are useful for treatment, prevention and diagnosis of hdm2-associated diseases, particularly tumours and leukemia, including use for passive or active immunisation. They can also be used to screen for therapeutic agents. This sequence encodes the polylinker Scat-Li-(Bsgfi-Scal) fragment used in the construction of the fusion constructs described in the disclosure of the invention

Sequence 115 BP; 19 A; 33 C; 47 G; 16 T; 0 U; 0 Other;

	Query Match	10.28;	Score 25.6;	DB 6;	Length 115;
	Best Local Similarity	52.99;	Pred. No. 1.4e+03;		
	Matches 55;	Conservative 0;	Mismatches 49;	Indels 0;	Gaps 0;
Qy	106	CTCAGTTTCGGCTCTCAGGTTTCGGCTCTCGCCCTCAGCTTTGAGGCCAGACAGCTCCGAG	165		
Db	9	CTTCGGTCCCGGCACCAAGGCTCAGGTTGCGCGCGAGGCAGCGCGCGCGGAGGACGCG	68		
Qy	166	TCGGGGCAGGAGGCGCGGGGAGAGACAGAGCGGCTCTCGCCCCCTT	209		
Db	69	CGCGCAGGAGGAGCGGTGCAGCAGAGTCTCTGCATCTCTTGAAGTACTT	112		

RESULT 2  
AEG19874/c  
ID AEG19874 standard; DNA; 96 BP.

XX	AEGL9874;	
AC		
XX		
DT	18-MAY-2006 (first entry)	
XX		
DE	Temp+ DNA..	
XX		
KW	ds; DNA amplification; ligase chain reaction; fluorescence;	
KW	DNA detection; diagnosis; mutagenesis; DNA sequencing.	
XX		
OS	Unidentified.	

XX  
PN  
XX  
PD

US2006057611-A1.  
16-MAR-2006.

XX  
PF 30-JUN-2005; 2005US-00173902.  
XX  
PR 30-JUN-2004; 2004US-0584665P.

PA (APPL-) APPLERA CORP.

PI Kao HP, Lao KQ, Jones R;

DR WPI; 2006-239070/25.

PT Quantitating target

PT amplifying exponenti

PS Example 2; SEQ ID NO 22; 34pp; English.

The present nucleic acid sequence was used in the current invention relating to quantitating target sequences by exponentially amplifying sequences in a reaction that terminates when a selected number of exponential amplicons are produced, linearly amplifying an exponential amplicon to produce linear amplicons in coupled reactions that produces a detectable signal proportional to a linear amplicon, and measuring fluorescence signals as a function of the amplification cycle number. The invention further relates to obtaining a cycle number (C<sub>e</sub>) and a copy number of a nucleic acid amplification reaction by exponentially and linearly amplifying a target sequence in a coupled reaction under conditions in which the exponential amplification terminates before reaching a plateau and a reporter molecule generates a detectable signal

proportional to the number of linear stranded amplicons, measuring the detectable signal as a function of cycle number, and obtaining from it the  $C_e$  value of the amplification reaction. The detectable signal is produced by a reporter molecule, where the reporter molecule is a self-quenching fluorescence probe, peptide nucleic acid (PNA) probe or 5'-nuclease or flap hydrolyzable probe. The target sequence is amplified in a thermal cycling reaction comprising forward and reverse amplification primers, hydrolyzable probe and thermostable polymerase having 5'-3' nuclease activity, where the forward primer is in excess of the reverse primer by at least 50:1, the probe hybridizes to a target sequence 3' relative to the forward primer, where the conditions of the reaction are effective for the forward primer, probe, and target sequence to form a substrate for the nuclease activity and for the nuclease activity to hydrolyze the probe to generate the detectable signal. The melting temperatures ( $T_m$ ) of the forward primer, reverse primer and probe with the target sequence are 5 degrees C or less. The conditions terminate the exponential phase at or before the cycle number that the exponential phase is capable of producing a detectable signal. The method is useful for amplifying one or more target polynucleotide sequences of an unknown polymer accurately, sensitively and specifically with high throughput capacity using array based assays or by single-strand conformational analysis, and in diagnosis or testing. Log-linear amplification may be used to produce templates for nucleic acid sequencing or for use in mutagenesis and gene expression analysis.

Sequence 96 BP; 20 A; 18 C; 40 G; 18 T; 0 U; 0 Other;

Query Match	10.0%	Score	25.2	DB	15	Length	96	
Best Local Similarity	60.0%	Pred. No.	1.7e+03					
Matches	42	Conservative	0	Mismatches	28	Indels	0	
							Gaps	0

69 TCTGGATGACAGAGTCTCTCTGA CTCCCTCTGCGACGGGCTGAGTTTCCGGCTCCAGGTTGG 128  
90 TCTCAGTCCCGAACCTCTGTGAGACACCTCTGTA TTTTTCGTGACGGGGTTCC 31

129 CGTGTGGCC 138  
Ov

30 CCGTTCCGCC 21

RESULT 3  
AEG19878

AEGL9878  
ID AEG

AA AEG19878:

DT 18-MAY-20

Temp - DNA.

ds: DNA an

XX  
XX  
DNA deletion[illegible]

FM XX  
USZ00003/011-AT.

FD  
XX  
16-MAR-2006.

XX  
FF  
30-NOV-67; 1105-00

XX  
FK  
30-JUN-2004; 200405-030400Z

PA (APPL-) APPLERA CORF.  
XX .  
XX .

FI  
XX

DR  
XX  
WFL; 2006-239070/23.

```

PT quantitating target sequences for e.g. diagnostics, complete exponentially
PT amplifying a target to form exponential amplicons, and linearly
.pt amplifying exponential amplicons to form linear amplicons.
xx

```

PS Example 2; SEQ ID NO 23; 34pp; English.

XX The present nucleic acid sequence was used in the current invention

CC relating to quantitating target sequences by exponentially amplifying

CC sequences in a reaction that terminates when a selected number of

CC exponential amplicons are produced, linearly amplifying an exponential

CC amplicon to produce linear amplicons in coupled reactions that produces a

CC detectable signal proportional to a linear amplicon, and measuring

CC fluorescence signals as a function of the amplification cycle number. The

CC invention further relates to obtaining a cycle number (Cn) and a copy

CC number of a nucleic acid amplification reaction by exponentially and

CC linearly amplifying a target sequence in a coupled reaction under

CC conditions in which the exponential amplification terminates before

CC reaching a plateau and a reporter molecule generates a detectable signal

CC proportional to the number of linear stranded amplicons, measuring the

CC detectable signal as a function of cycle number, and obtaining from it

CC the Cn value of the amplification reaction. The detectable signal is

CC produced by a reporter molecule, where the reporter molecule is a self-

CC quenching fluorescence probe, peptide nucleic acid (PNA) probe or 5'-

CC nuclease or flap hydrolyzable probe. The target sequence is amplified in

CC a thermal cycling reaction comprising forward and reverse amplification

CC primers, hydrolyzable probe and thermostable polymerase having 5'-3'

CC nuclease activity, where the forward primer is in excess of the reverse

CC primer by at least 50:1, the probe hybridizes to a target sequence 3'

CC relative to the forward primer, where the conditions of the reaction are

CC effective for the forward primer, probe, and target sequence to form a

CC substrate for the nuclease activity and for the nuclease activity to

CC hydrolyze the probe to generate the detectable signal. The melting

CC temperatures (Tm) of the forward primer, reverse primer and probe with

CC the target sequence are 5 degrees C or less. The conditions terminate the

CC exponential phase at or before the cycle number that the exponential

CC phase is capable of producing a detectable signal. The method is useful

CC for amplifying one or more target polynucleotide sequences of an unknown

CC polymer accurately, sensitively and specifically with high throughput

CC capacity using array based assays or by single-strand conformational

CC analysis, and in diagnosis or testing. Log-linear amplification may be

CC used to produce templates for nucleic acid sequencing or for use in

CC mutagenesis and gene expression analysis. Note: The present sequence is

CC not shown in the patent but is a version of ABG19875 in the reverse (5'-

CC 3') orientation.

XX

SQ Sequence 96 BP; 18 A; 40 C; 18 G; 20 T; 0 U; 0 Other;

Query Match 10.0%; Score 25.2; DB 15; Length 96;

Best Local Similarity 60.0%; Pred. No. 1.7e+03;

Matches 42; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 69 TCTGGATGAGAGTCTCTGATCCCTCTGCGCAGGGCTGAGTTTCCGGCTCCAGGTTCG 128

DB 7 TCCAGCTCCCGAACCTCTGTGAGACCTCAGCAACCTCTGTATTTTCGGTGACCGGTTC 66

QY 129 CGTGTGCGCC 138

DB 67 CGCTTCGCC 76

RESULT 4

AAC11989

ID AAC11989 standard; cDNA; 92 BP.

XX

AC AAC11989;

XX

DT 06-OCT-2000 (first entry)

XX

DE Human secreted protein 5' EST; SEQ ID NO: 16064.

XX

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

KW gene therapy; chromosome mapping; ss.

KW

XX Homo sapiens.

OS

XX EP1033401-A2.

PN

XX

PD 06-SEP-2000.

XX

PF 21-FEB-2000; 2000EP-00200610.

XX

PR 26-FEB-1999; 99US-0122487P.

XX

PA (GEST ) GENSET.

XX

PI Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

DR

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for

PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for

PT diagnostic, forensic, gene therapy and chromosome mapping procedures.

PS

XX Claim 1; SEQ ID NO 16064; 71pp + Sequence Listing; English.-

CC The present sequence is one of a large number of 5' ESTs derived from

CC mRNAs encoding secreted proteins. No ORF has yet been conclusively

CC identified within the present sequence. The 5' ESTs were prepared from

CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST

CC sequences usually correspond mainly to the 3' untranslated region (UTR)

CC of the mRNA because they are often obtained from oligo-dT primed cDNA

CC libraries. Such ESTs are not well suited for isolating cDNA sequences

CC derived from the 5' ends of mRNAs and even in those cases where longer

CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'

CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used

CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in

CC diagnostic, forensic, gene therapy and chromosome mapping procedures.

CC They are used to obtain upstream regulatory sequences and to design

CC expression and secretion vectors

XX

SQ Sequence 92 BP; 19 A; 24 C; 44 G; 5 T; 0 U; 0 Other;

Query Match 9.8%; Score 24.8; DB 3; Length 92;

Best Local Similarity 67.3%; Pred. No. 2.2e+03;

Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 156 CAGTCTCGAGTCGGCGGAGGGGGGGGAGAGACGAGCGGCTCTGGCCCC 207

DB 13 CAGCTCGAATCGGAGCGGAAACAGCGGGGCTGGGAGCGGCGGCGGCCCC 64

RESULT 5

ABV03167

ID ABV03167 standard; cDNA; 103 BP.

XX

AC ABV03167;

XX

DT 13-SEP-2002 (first entry)

XX

DE Human prostate expression marker cDNA 3158.

XX

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

KW pharmacogenomic marker; gene; ss.

KW

XX Homo sapiens.

OS

XX WO200160860-A2.

PN

XX

PD 23-AUG-2001.

XX

PF 20-FEB-2001; 2001WO-US005171.

XX

XX 17-FEB-2000; 2000US-0183319P.

PR 16-MAR-2000; 2000US-0189862P.

PR 25-MAY-2000; 2000US-0207454P.

PR 09-JUN-2000; 2000US-0211314P.

PR 18-JUL-2000; 2000US-0219007P.

PR 13-DEC-2000; 2000US-0255281P.

XX

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.





Query Match 9.4%; Score 23.6; DB 3; Length 72;  
Best Local Similarity 69.6%; Pred. No. 4.7e+03;  
Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 128 GCGGTGCGCTGAGGTTTGGAGCCAGACAGCTCGCAGTCGGGCGAG 173  
DB 58 GCGTGGGCGCCGGGGATCGAGGGGATCCAGACAGAGCGGCGCCAG 13

## RESULT 10

AAH68919

ID AAH68919 standard; cDNA; 97 BP.

XX AC

XX AC

XX AC

XX 19-SEP-2001 (first entry)

XX AC

XX Human cervical cancer marker nucleic acid 193.

XX AC

XX Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.

XX AC

XX Homo sapiens.

XX AC

XX WO200142457-A2.

XX AC

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

XX PD

ACD69745/c

ID ACD69745 standard; DNA; 100 BP.

XX AC

XX AC

XX 18-SEP-2003 (first entry)

XX AC

XX E. coli K12 MG1555 biochip probe SEQ ID 1015.

XX AC

XX Biochip; gene expression; gut; diagnostic; detection; probe; ss.

XX AC

XX Escherichia coli.

XX AC

XX EP1260592-A1.

XX AC

XX 27-NOV-2002.

XX AC

XX 17-MAY-2001; 2001EP-001121179.

XX AC

XX 17-MAY-2001; 2001EP-001121179.

XX AC

XX (MWGB-) MWG-BIOTECH AG.

XX AC

XX Donner H, Drescher B, Huber A, Weber J;

XX AC

XX WPI; 2003-241155/24.

XX AC

XX Biochip containing probes complementary with open reading frames in Escherichia coli K12, useful for detecting gene expression and expression patterns.

XX AC

XX Claim 3; Page 168; 2004pp; German.

XX AC

XX This invention describes a novel biochip comprising probe spots, each containing many identical probes. The probes are nucleotide sequences of 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at least one includes a segment of at least 20 bases identical with, or complementary to, a segment of an open reading frame (orf) of Escherichia coli K12. The biochip is used for specific detection of gene expression in K12 and for determining the gene expression pattern, e.g. for diagnostic determination of which E. coli strains are present in the gut, and to determine the effects of e.g. growth media on gene expression. The biochip provides as comprehensive as possible detection of the K12 genome, with simultaneous analysis of many different genes with a single device, and comparison of gene expression between K12 and its mutants or other E. coli strains in a single experiment. Apart from qualitative and quantitative information about gene expression, it also allows measurements of population densities for the various strains. The use of synthetic oligonucleotides for preparation of probes allows free variation in probe length and ensures high purity (and thus selectivity, reactivity and reproducibility); also synthetic probes are generally shorter than probes prepared by polymerase chain reaction. ACD68731 to ACD81540 represent oligonucleotide probes used with the biochip described in the invention

XX AC

XX Sequence 100 BP; 21 A; 29 C; 38 G; 12 T; 0 U; 0 Other;

XX AC

XX Query Match 9.3%; Score 23.4; DB 8; Length 100;

XX AC

XX Best Local Similarity 63.2%; Pred. No. 5.8e+03;

XX AC

XX Matches 36; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

XX AC

QY 100 CACGGGCTGAGTTTCGGCTCCAGGTTCCGGTTCCTCCCTAGGTTTGGCCAGAC 156

DB 88 CAGTTCTCGCGCGCTGACCATGTTCGCCAGTCCGCGGGTTTCTGCCAGCC 32

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

Query Match 9.4%; Score 23.6; DB 3; Length 72;

Best Local Similarity 69.6%; Pred. No. 4.7e+03;

Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 128 GCGGTGCGCTGAGGTTTGGAGCCAGACAGCTCGCAGTCGGGCGAG 173

DB 58 GCGTGGGCGCCGGGGATCGAGGGGATCCAGACAGAGCGGCGCCAG 13

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

## RESULT 11

AAH68919

ID AAH68919 standard; cDNA; 97 BP.

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

Query Match 9.4%; Score 23.6; DB 3; Length 72;

Best Local Similarity 69.6%; Pred. No. 4.7e+03;

Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 128 GCGGTGCGCTGAGGTTTGGAGCCAGACAGCTCGCAGTCGGGCGAG 173

DB 58 GCGTGGGCGCCGGGGATCGAGGGGATCCAGACAGAGCGGCGCCAG 13

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX DE E. coli K12 MG1655 biochip probe SEQ ID 7863.  
 XX DE Biochip; gene expression; gut; diagnostic; detection; probe; ss.  
 XX KW Escherichia coli.  
 XX OS EPI260592-A1.  
 XX PN 27-NOV-2002.  
 XX PD 17-MAY-2001; 2001EP-00112179.  
 XX PF 17-MAY-2001; 2001EP-00112179.  
 XX PR (MWGB-) MWG-BIOTECH AG.  
 XX PA Donner H, Drescher B, Huber A, Weber J;  
 XX PI WPI; 2003-241155/24.  
 XX DR Biochip containing probes complementary with open reading frames in  
 XX PT Escherichia coli K12, useful for detecting gene expression and expression  
 XX PT patterns.  
 XX PS Claim 3; Page 1228; 2004pp; German.  
 XX CC This invention describes a novel biochip comprising probe spots, each  
 CC containing many identical probes. The probes are nucleotide sequences of  
 CC 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at  
 CC least one includes a segment of at least 20 bases identical with, or  
 CC complementary to, a segment of an open reading frame (orf) of Escherichia  
 CC coli K12. The biochip is used for specific detection of gene expression  
 CC in K12 and for determining the gene expression pattern, e.g. for  
 CC diagnostic determination of which E. coli strains are present in the gut,  
 CC and to determine the effects of e.g. growth media on gene expression. The  
 CC biochip provides as comprehensive as possible detection of the K12  
 CC genome, with simultaneous analysis of many different genes with a single  
 CC device, and comparison of gene expression between K12 and its mutants or  
 CC other E. coli strains in a single experiment. Apart from qualitative and  
 CC quantitative information about gene expression, it also allows  
 CC measurements of population densities for the various strains. The use of  
 CC synthetic oligonucleotides for preparation of probes allows free  
 CC variation in probe length and ensures high purity (and thus selectivity,  
 CC reactivity and reproducibility); also synthetic probes are generally  
 CC shorter than probes prepared by polymerase chain reaction. ACD8731 to  
 CC ACD81540 represent oligonucleotide probes used with the biochip described  
 CC in the invention  
 XX SQ Sequence 100 BP; 13 A; 35 C; 29 G; 23 T; 0 U; 0 Other;  
 Query Match 9.3%; Score 23.4; DB 8; Length 100;  
 Best Local Similarity 63.2%; Pred. No. 5.8e+03;  
 Matches 36; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
 QY 100 CACGGCTGAGTTCCGGCTCCAGGTTCGGCTGCGCCCTGAGTTTGGAGCCAGAC 156  
 DB 43 CAGTTCTGCGCGCTGCACCATGTTCCAGTGCCTGCGCGGGTTCGCGCAGCC 99  
 RESULT 13  
 ID ADR28210  
 XX ADR28210 standard; DNA; 100 BP.  
 AC ADR28210.  
 XX 04-NOV-2004 (first entry)  
 DT Oligonucleotide Dmeter, SEQ ID 9.  
 DE 2-amino-4-alkylthio-butylric acid; methionine synthase;  
 KW cystathionine-gamma-synthase; acylhomoserine sulphydrylase; ss.  
 XX

OS Synthetic.  
 XX FR2851255-A1.  
 XX PD 20-AUG-2004.  
 XX PF 14-MAY-2003; 2003FR-00005768.  
 XX PR 18-FEB-2003; 2003FR-00001924.  
 XX PA (META-) METABOLIC EXPLORER.  
 XX PI Chateau M, Gonzales B, Soucaille PNP;  
 XX DR WPI; 2004-618123/60.  
 XX PT New strains of microorganisms that produce 2-amino-4-alkylthio-butylric  
 PT acid, useful for preparing L-methionine, from simple carbon source and a  
 PT mercaptan or its salt, have modified methionine synthase activity.  
 XX PS Example 1; SEQ ID NO 9; 68pp; French.  
 XX CC The present invention relates to a novel strain (A) of a microorganism  
 CC which produces a 2-amino-4-alkylthio-butylric acid (I) by metabolising a  
 CC simple sugar and a thiol (III), or its salt, and has at least one gene  
 CC encoding an enzyme with modified methionine synthase (MS) activity. (A)  
 CC are specifically used for fermentative production of L-methionine, which  
 CC is produced from a simple carbon source and alkylmercaptan, i.e.  
 CC synthesis of L-Met is independent of synthesis of cysteine; the methyl  
 CC mercaptan used is a toxic waste product from the petrochemical industry  
 CC and synthesis of L-Met occurs in a single step from O-(acetyl or  
 CC succinyl)-L-homoserine. The enzyme with modified MS activity is either  
 CC cystathionine-gamma-synthase or an acylhomoserine sulphydrylase, and is  
 CC modified so that the substrate is reacted with (II) rather than with L-  
 CC cysteine, to result in preferential conversion of the substrate to (I) or  
 CC homocysteine. The present sequence was used in an example from the  
 CC invention.  
 XX SQ Sequence 100 BP; 15 A; 36 C; 25 G; 24 T; 0 U; 0 Other;  
 Query Match 9.3%; Score 23.4; DB 13; Length 100;  
 Best Local Similarity 63.2%; Pred. No. 5.8e+03;  
 Matches 36; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
 QY 100 CACGGCTGAGTTTCCGGCTCCAGGTTCGGCTGCGCCCTGAGTTTGGAGCCAGAC 156  
 DB 12 CAGTTCTGCGCGCTGCACCATGTTCCAGTGCCTGCGCGGGTTCGCGCAGCC 68  
 RESULT 14  
 ID ADR99734  
 XX ADR99734 standard; DNA; 100 BP.  
 AC ADR99734.  
 XX 02-DEC-2004 (first entry)  
 DT Nucleic acid Dmeter to generate evolved microorganisms.  
 DE ss; microorganism evolution; metabolic pathway; metabolite;  
 KW biotransformation; NADPH-dependent enzyme; nucleic acid metabolism;  
 KW lipid metabolism; sugar metabolism.  
 XX Unidentified.  
 XX WO2004076659-A2.  
 XX PD 10-SEP-2004.  
 XX PF 17-FEB-2004; 2004WO-FR000354.  
 XX PR 18-FEB-2003; 2003FR-00001924.  
 XX PR 14-MAY-2003; 2003FR-00005768.

```
PR 14-MAY-2003; 2003FR-00005769.
PR 06-NOV-2003; 2003FR-00013054.
PA (META-) METABOLIC EXPLORER.
XX
XX Chateau M, Gonzalez B, Meynial-Salles I, Soucaille PNP, Zink O;
PI
XX WPI; 2004-653418/63.
XX
XX New evolved microorganisms with altered metabolic pathways, useful e.g.
XX for production of amino acids, are selected as mutants able to grow on
XX defined media.
XX
XX Disclosure; SEQ ID NO 1; 113pp; French.
XX
XX The invention relates to a method for preparing evolved microorganisms
XX (A) with modified metabolic pathways comprising: (a) genetic modification
XX of a microorganism to inhibit production or consumption of a metabolite
XX when it is grown on a defined medium, thus affecting its ability to grow;
XX (b) growing the modified organism in the defined medium so that evolution
XX can occur, optionally with addition of a co-substrate to allow evolution;
XX and (c) selecting as (A) cells able to grow on the medium, optionally in
XX presence of co-substrate. The evolved microorganisms (A), or evolved
XX proteins (I) expressed by them, are useful in biotransformation
XX processes, especially those involving NADPH-dependent enzymes,
XX particularly synthesis of amino acids (Met, Cys, Thr, Lys or Ile) but
XX also synthesis of nucleic acids or lipids, and metabolism of sugars. (A)
XX provide more efficient production of selected metabolites than parent
XX strains. This sequence represents a nucleic acid molecule used in the
XX method of the invention.
XX
XX Sequence 100 BP; 15 A; 36 C; 25 G; 24 T; 0 U; 0 Other;
SQ
Query Match 9.3%; Score 23.4; DB 13; Length 100;
Best Local Similarity 63.2%; Pred. No. 5.8e+03;
Matches 36; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
Oy 100 CACGGGTGAGTTTCGGGCTCCAGGTCGCGTGTCGCCCTGAGGTTTGAGGCCAGAC 156
Db 12 CAAATTCTGCCCGCCCTGCACCAATGTCGCCAGTCCGCGCGGGTTCTGCGCCGCC 68
RESULT 15
AAZ89260/C
ID AAZ89260 standard; DNA; 59 BP.
XX
XX AAZ89260;
XX
XX 09-JUN-2000 (first entry)
XX
XX Human embryonic brain protein PCR primer #5.
XX
XX Human; brain; nerve degeneration; neurotropic; neuroprotective;
XX anticonvulsant; antiparkinsonian; antidiabetic; treatment; infarction;
XX parkinson's disease; Alzheimer's disease; Huntington's disease;
XX muscular hypoplastic lateral sclerosis; diabetic neuropathy; PCR primer;
XX ss.
XX
XX Homo sapiens.
XX
XX WO200007614-A1.
XX
XX 17-FEB-2000.
XX
XX 02-AUG-1999; 99WO-JP004171.
XX
XX 05-AUG-1998; 98JP-00221886.
XX
XX 05-FEB-1999; 99JP-00029164.
XX
XX (SAKA) OTSUKA PHARM CO LTD.
XX
XX Horie M, Hirano H, Kyushiki H, Mitaumoto Y, Mori A, Watanabe A;
PI
XX
```

```
DR WPI; 2000-205568/18.
XX
XX New protein isolated from human embryonic brain useful for treating nerve
XX degeneration diseases e.g. Parkinson's diseases and Alzheimer's disease.
XX
XX Example 2; Page 62; 69pp; Japanese.
XX
XX This invention describes a novel human embryonic brain derived protein
XX (I) which has neurotropic, neuroprotective, anticonvulsant,
XX antiparkinsonian and antidiabetic activity. (I) is useful for treating
XX nerve degeneration diseases e.g. Parkinson's disease, Alzheimer's
XX disease, muscular hypoplastic lateral sclerosis, Huntington's disease,
XX brain infarction, diabetic neuropathy and traumatic nerve degeneration.
XX AAZ89256-289234 represent PCR primers used in the isolation and
XX amplification of the human brain protein described in the method of the
XX invention.
XX
XX Sequence 59 BP; 9 A; 23 C; 14 G; 13 T; 0 U; 0 Other;
SQ
Query Match 9.2%; Score 23.2; DB 3; Length 59;
Best Local Similarity 65.4%; Pred. No. 5.8e+03;
Matches 34; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
Oy 159 CTCGACGTCGGGCGGAGGGGGGGGAGAGAGAGAGCGGCTCTGCGCCCTTA 210
Db 52 CTGGCAGTCGCTCAGGGGAGGTCCGGAAAGAGCAGCCAGCTTAACCGGGCGGCA 1
Search completed: June 19, 2007, 13:36:55
Job time : 376 secs
```



Result No.	Score	Query			DB	ID	Description
		Match	Length	Count			
1	24.8	9.8	92	3	US-09-513-999C-16064	Sequence 16064, A	
2	24.2	9.6	96	3	US-09-210-305C-1	Sequence 1, Appl	
C 3	23.8	9.4	78	3	US-09-877-243A-145	Sequence 145, App	
C 4	23.8	9.4	78	3	US-09-877-705A-145	Sequence 145, App	
C 5	23.8	9.4	78	3	US-09-877-738C-145	Sequence 145, App	
C 6	23.6	9.4	72	3	US-09-513-999C-15065	Sequence 15065, A	
C 7	22.6	9.0	66	3	US-09-866-108A-15685	Sequence 15685, A	
8	22.4	8.9	119	3	US-09-513-999C-23785	Sequence 23785, A	
9	22.2	8.8	67	3	US-09-513-999C-15277	Sequence 15277, A	
C 10	22.2	8.8	102	3	US-09-347-613C-13	Sequence 13, Appl	
C 11	22.2	8.8	102	3	US-09-662-183A-13	Sequence 13, Appl	
C 12	22.2	8.8	113	3	US-09-367-927A-1	Sequence 1, Appl	
C 13	22.2	8.8	115	3	US-09-513-999C-20278	Sequence 20278, A	
C 14	21.8	8.7	86	2	US-07-964-624D-57	Sequence 57, Appl	
C 15	21.8	8.7	86	2	US-08-442-062-57	Sequence 57, Appl	
C 16	21.8	8.7	86	2	US-08-748-697A-57	Sequence 57, Appl	
C 17	21.8	8.7	86	3	US-09-165-616-57	Sequence 57, Appl	
C 18	21.8	8.7	86	3	US-10-040-497-57	Sequence 57, Appl	
C 19	21.8	8.7	93	3	US-09-902-540-4514	Sequence 4514, Ap	
C 20	21.8	8.7	104	3	US-09-513-999C-29691	Sequence 29691, A	
C 21	21.8	8.7	107	3	US-09-621-976-9492	Sequence 9492, A	
C 22	21.6	8.6	51	3	US-09-513-999C-14603	Sequence 14603, A	
C 23	21.6	8.6	116	2	US-08-458-423A-34	Sequence 34, Appl	



COUNTRY: U.S.A.  
 ZIP: 06510-2802  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage  
 COMPUTER: IBM  
 OPERATING SYSTEM: WINDOWS 95/98  
 SOFTWARE: MS WORD  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/210.305C  
 FILING DATE: 11-Dec-1998  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 96 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: oligonucleotide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-09-210-305C-1

Query Match 9.6%; Score 24.2; DB 3; Length 96;  
 Best Local Similarity 43.5%; Pred. No. 5.6e+02;  
 Matches 30; Conservative 11; Mismatches 28; Indels 0; Gaps 0;  
 QY 32 GCGCTCCCAAGTTGGAAGGCGCTTTGCTTCTGTTTCTGGATGCAGAGTCCTCTGACT 91  
 Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
 10 GCGCCUGCAAGCGAAUUGCGUGGCUCCUGGCUACGCGCUGUGGCGGACUGCCU 69  
 QY 92 CCCTCTGCC 100  
 Db |||||  
 70 GCUGCUGCC 78

RESULT 3  
 US-09-877-243A-145/c  
 ; Sequence 145, Application US/09877243A  
 ; Patent No. 6696256  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Li, Jason  
 ; TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED  
 ; FILE REFERENCE: 26757-702  
 ; CURRENT APPLICATION NUMBER: US/09/877,243A  
 ; CURRENT FILING DATE: 2001-08-16  
 ; NUMBER OF SEQ ID NOS: 162  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 145  
 ; LENGTH: 78  
 ; TYPE: DNA  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Hybridization probe MP74  
 US-09-877-243A-145

Query Match 9.4%; Score 23.8; DB 3; Length 78;  
 Best Local Similarity 59.7%; Pred. No. 7e+02;  
 Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;  
 QY 109 AGTTTCGGCTCCAGGTCGCGTGTGCGCCCTGAGTTTGAGGCCAGACAGCTCGCAGTCG 168  
 Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
 78 AGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTCAG 19  
 QY 169 GGCAGGG 175  
 Db |||||  
 18 GTCAGAG 12

RESULT 4  
 US-09-877-705A-145/c  
 ; Sequence 145, Application US/09877705A  
 ; Patent No. 6821737  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Li, Jason

; TITLE OF INVENTION: METHOD FOR SCREENING FOR DRUG CANDIDATES FOR MODULATING TRANSCRIPTION  
 ; TITLE OF INVENTION: FACTOR ACTIVITY  
 ; FILE REFERENCE: 26757-704  
 ; CURRENT APPLICATION NUMBER: US/09/877,705A  
 ; CURRENT FILING DATE: 2001-08-16  
 ; NUMBER OF SEQ ID NOS: 162  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 145  
 ; LENGTH: 78  
 ; TYPE: DNA  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Hybridization probe MP74  
 US-09-877-705A-145

Query Match 9.4%; Score 23.8; DB 3; Length 78;  
 Best Local Similarity 59.7%; Pred. No. 7e+02;  
 Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;  
 QY 109 AGTTTCGGCTCCAGGTCGCGTGTGCGCCCTGAGTTTGAGGCCAGACAGCTCGCAGTCG 168  
 Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
 78 AGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTCAG 19  
 QY 169 GGCAGGG 175  
 Db |||||  
 18 GTCAGAG 12

RESULT 5  
 US-09-877-738C-145/c  
 ; Sequence 145, Application US/09877738C  
 ; Patent No. 6924113  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Li, Jason  
 ; TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED  
 ; FILE REFERENCE: 26757-701  
 ; CURRENT APPLICATION NUMBER: US/09/877,738C  
 ; CURRENT FILING DATE: 2001-06-08  
 ; NUMBER OF SEQ ID NOS: 162  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 145  
 ; LENGTH: 78  
 ; TYPE: DNA  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Hybridization probe MP74  
 US-09-877-738C-145

Query Match 9.4%; Score 23.8; DB 3; Length 78;  
 Best Local Similarity 59.7%; Pred. No. 7e+02;  
 Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;  
 QY 109 AGTTTCGGCTCCAGGTCGCGTGTGCGCCCTGAGTTTGAGGCCAGACAGCTCGCAGTCG 168  
 Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
 78 AGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTCAG 19  
 QY 169 GGCAGGG 175  
 Db |||||  
 18 GTCAGAG 12

RESULT 6  
 US-09-513-999C-15065/c  
 ; Sequence 15065, Application US/09513999C  
 ; Patent No. 6783961  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dumas Milne Edwards, J.B.  
 ; APPLICANT: Duclert, A.  
 ; APPLICANT: Giordano, J.Y.  
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
 ; Patent No. 6783961  
 ; FILE REFERENCE: 59.US2.REG

[illegible]

```

; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-662-183A-13

Query Match      8.8%; Score 22.2; DB 3; Length 102;
Best Local Similarity 61.0%; Pred. No. 2.4e+03;
Matches 36; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 149 GGCACACAGCTCGCAGTCCGGCAGGAGGGGGGGGAGAGACGAGCGGCTCTGGCCCC 207
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 74 GGCAGCAGGGCTGGCTGACGGCGGGGAGACCCCGGGGGCGGTTCGACGGCCCCGGCGCCC 16

RESULT 12
US-09-367-927A-1/c
; Sequence 1, Application US/09367927A
; Patent No. 6300126
; GENERAL INFORMATION:
; APPLICANT: GRUMMT, INGRID
; APPLICANT: RAINWEG, MITTLERER
; APPLICANT: GRUMMT, FRIEDERICK
; APPLICANT: VAN DER VOGELWEIDE STRASSE, WALTHER
; TITLE OF INVENTION: EXPRESSION VECTOR FOR THE PERMANENT
; TITLE OF INVENTION: EXPRESSION OF FOREIGN DNA
; FILE REFERENCE: 35280043US00
; CURRENT APPLICATION NUMBER: US/09/367,927A
; CURRENT FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 113
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-367-927A-1

Query Match      8.8%; Score 22.2; DB 3; Length 113;
Best Local Similarity 64.7%; Pred. No. 2.4e+03;
Matches 33; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 147 GAGGCCACAGACGCTCGCAGTCCGGCAGGAGGGCGGGGAGAGACGAGCGG 197
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 66 GTGGCCCCCGCGCTCCGCGCGGGGGGGGGGGGGGGGAGACACTTTCGG 16

RESULT 13
US-09-513-999C-20278/c
; Sequence 20278, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.Pm
; SEQ ID NO 20278
; LENGTH: 115
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-20278

Query Match      8.8%; Score 22.2; DB 3; Length 115;
Best Local Similarity 61.0%; Pred. No. 2.4e+03;
Matches 36; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 169 GGCAGGAGGGCGGGGAGACGAGCGGCTCTGGCCCCCTTAATTGTACTTCGGGCTCG 227
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Db 63 GGGTGGGGCCCGGAGAGACAGCAGCCTCGAGCCAGAGATTTGTTTCGTTTCG 5

RESULT 14

US-07-964-624D-57/c  
; Sequence 57, Application US/07964624D  
; Patent No. 5496938  
; GENERAL INFORMATION:  
; APPLICANT: GOLD, LARRY M.  
; APPLICANT: TUERK, CRAIG  
; TITLE OF INVENTION: METHOD OF SELECTING NUCLEIC  
; TITLE OF INVENTION: ACIDS ON THE BASIS OF  
; TITLE OF INVENTION: STRUCTURE  
; NUMBER OF SEQUENCES: 83  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Swanson & Bratschun, L.L.C.  
; STREET: 8400 E. Prentice Avenue, Suite 200  
; CITY: Englewood  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80111

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3 1/5 inch, 1.44 MB  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/964,624D  
; FILING DATE: 21-OCTOBER-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/714,131  
; FILING DATE: 10-JUNE-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/536,428  
; FILING DATE: 11-JUNE-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barry J. Swanson  
; REGISTRATION NUMBER: 33,215  
; REFERENCE/DOCKET NUMBER: NEX05  
; TELEPHONE: (303) 793-3333  
; TELEFAX: (303) 793-3433  
; INFORMATION FOR SEQ ID NO: 57:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 86 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-07-964-624D-57

Query Match 8.7%; Score 21.8; DB 2; Length 86;  
Best Local Similarity 56.2%; Pred. No. 3e+03;  
Matches 41; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 84 CTCGACTCCCTCGCAGCGGCTGAGTTCCGGCTCCAGGTTCCGGTGCCTGAGG 143  
Db 86 CCGGATCCTCTTTACTCTGTGTGAGCTCCAGAGTCCACTATCGTGTTCGATGGAG 27

Qy 144 TTTGAGGCCAGAC 156  
Db 26 TTGTCGGAAGGC 14

RESULT 15

US-08-442-062-57/c  
; Sequence 57, Application US/08442062  
; Patent No. 5595877  
; GENERAL INFORMATION:  
; APPLICANT: GOLD, LARRY M.  
; APPLICANT: TUERK, CRAIG  
; TITLE OF INVENTION: METHOD OF SELECTING NUCLEIC  
; TITLE OF INVENTION: ACIDS ON THE BASIS OF

TITLE OF INVENTION: STRUCTURE  
; NUMBER OF SEQUENCES: 83  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Swanson & Bratschun, L.L.C.  
; STREET: 8400 E. Prentice Avenue, Suite 200  
; CITY: Englewood  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3 1/5 inch, 1.44 MB  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/442,062  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/964,624  
; FILING DATE: 21-OCTOBER-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/714,131  
; FILING DATE: 10-JUNE-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/536,428  
; FILING DATE: 11-JUNE-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barry J. Swanson  
; REGISTRATION NUMBER: 33,215  
; REFERENCE/DOCKET NUMBER: NEX05/D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 793-3333  
; TELEFAX: (303) 793-3433  
; INFORMATION FOR SEQ ID NO: 57:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 86 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-442-062-57

Query Match 8.7%; Score 21.8; DB 2; Length 86;  
Best Local Similarity 56.2%; Pred. No. 3e+03;  
Matches 41; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 84 CTCGACTCCCTCGCAGCGGCTGAGTTCCGGCTCCAGGTTCCGGTGCCTGAGG 143  
Db 86 CCGGATCCTCTTTACTCTGTGTGAGCTCCAGAGTCCACTATCGTGTTCGATGGAG 27

Qy 144 TTTGAGGCCAGAC 156  
Db 26 TTGTCGGAAGGC 14

Search completed: June 19, 2007, 13:59:35  
Job time : 424 secs

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 13:37:11 ; Search time 3937 Seconds  
(without alignments)  
786.509 Million cell updates/sec

Title: US-10-604-726A-8797  
Perfect score: 252  
Sequence: 1 999ttatctgcaactgagag.....tctctcttttgcacactcc 252

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 1892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 24482366

Minimum DB seq length: 0  
Maximum DB seq length: 120

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_NA\_Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq:\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq:\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	27	10.7	67	11	US-10-310-914A-16611
C 2	25.2	10.0	96	16	US-11-173-902-22/c
C 3	25.2	10.0	109	9	US-10-674-124A-16551
C 4	24.6	9.8	103	9	US-10-357-930-3158
C 5	24.6	9.8	104	9	US-10-357-930-12327
C 6	24.2	9.6	105	6	US-10-106-698-3252
C 7	24	9.5	93	11	US-10-310-914A-17067
C 8	23.8	9.4	78	3	US-09-877-705A-145
C 9	23.8	9.4	78	3	US-09-947-274-145
C 10	23.8	9.4	78	3	US-09-877-738A-145
C 11	23.8	9.4	78	4	US-09-877-403A-145
C 12	23.8	9.4	78	8	US-10-779-595-145
C 13	23.4	9.3	100	10	US-10-781-499-1
C 14	23.4	9.3	120	3	US-09-796-692-6323
C 15	23.4	9.3	120	6	US-10-040-862-6323
C 16	23.4	9.3	120	7	US-10-057-475B-6323
C 17	23.4	9.3	120	7	US-10-154-884B-6323

18	23.4	9.3	120	9	US-10-764-324-6323	Sequence 6323, Ap
C 19	23.2	9.2	101	3	US-09-864-761-27544	Sequence 27544, A
C 20	23.2	9.2	118	7	US-10-029-386-21226	Sequence 21226, A
C 21	23	9.1	65	3	US-09-908-975-792	Sequence 792, App
C 22	23	9.1	87	3	US-09-294-093B-4883	Sequence 4883, App
C 23	22.8	9.0	60	3	US-09-908-975-16455	Sequence 16455, A
C 24	22.6	9.0	66	3	US-09-866-108-15685	Sequence 15685, A
C 25	22.6	9.0	66	8	US-10-723-361-15685	Sequence 15685, A
C 26	22.4	8.9	116	9	US-10-425-115-142012	Sequence 142012, A
C 27	22.2	8.8	102	3	US-09-804-615-13	Sequence 13, Appl
C 28	22.2	8.8	102	8	US-10-661-984A-13	Sequence 13, Appl
C 29	22.2	8.8	102	9	US-10-806-793-13	Sequence 387, App
C 30	22	8.7	68	10	US-10-490-955-387	Sequence 387, App
C 31	22	8.7	68	11	US-10-310-914A-2865	Sequence 2865, Ap
C 32	22	8.7	68	11	US-10-310-914A-3692	Sequence 3692, Ap
C 33	22	8.7	89	10	US-10-909-125-1425	Sequence 1425, Ap
C 34	22	8.7	99	11	US-10-310-914A-817	Sequence 817, App
C 35	22	8.7	104	8	US-10-242-535A-9222	Sequence 9222, Ap
C 36	22	8.7	104	8	US-10-085-783A-9222	Sequence 9222, Ap
C 37	22	8.7	113	3	US-09-864-761-21889	Sequence 21889, A
C 38	22	8.7	116	11	US-10-310-914A-12025	Sequence 12025, A
C 39	21.8	8.7	63	11	US-10-310-914A-20336	Sequence 20336, A
C 40	21.8	8.7	86	6	US-10-040-497-57	Sequence 57, Appl
C 41	21.8	8.7	86	9	US-10-818-954-57	Sequence 57, Appl
C 42	21.8	8.7	96	3	US-09-918-063-32	Sequence 32, Appl
C 43	21.8	8.7	96	3	US-09-918-063-34	Sequence 34, Appl
C 44	21.8	8.7	111	3	US-09-864-761-23937	Sequence 23937, A
C 45	21.8	8.7	113	3	US-09-933-797-725	Sequence 725, App

## ALIGNMENTS

### RESULT 1

US-10-310-914A-16611/c  
; Sequence 16611, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiller, Kruzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 16611  
; LENGTH: 67  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-16611

Query Match 10.7%; Score 27; DB 11; Length 67;  
Best Local Similarity 85.7%; Pred. No. 2e+02;  
Matches 30; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy	174	GGAGGGGGGGGAGAGAGAGCGGCTCTGGGCCCT 208
Db	67	GGAGGGTGGGGAGAGAGAGCCCTGGGCCCT 33

### RESULT 2

US-11-173-902-22/c  
; Sequence 22, Application US/11173902  
; Publication No. US20060057611A1  
; GENERAL INFORMATION:  
; APPLICANT: KAO, H. PIN  
; APPLICANT: LAO, KAI QIN  
; APPLICANT: JONES, ROBERT  
; TITLE OF INVENTION: LOG-LINEAR AMPLIFICATION  
; FILE REFERENCE: 375461-021US  
; CURRENT APPLICATION NUMBER: US/11/173,902



```

RESULT 6
US-10-106-698-3252
, Sequence 3252, Application US/10106698
, Publication No. US2003010960A1
, GENERAL INFORMATION:
, APPLICANT: Ruben et al.
, TITLE OF INVENTION: Colon and Colon Cancer
, FILE REFERENCE: PA00591
, CURRENT APPLICATION NUMBER: US/10/106,698
, CURRENT FILING DATE: 2002-03-27
, PRIOR APPLICATION NUMBER: PCT/US00/26524
, PRIOR FILING DATE: 2000-09-28
, PRIOR APPLICATION NUMBER: US 60/157,137
, PRIOR FILING DATE: 1999-09-29
, PRIOR APPLICATION NUMBER: US 60/163,280
, PRIOR FILING DATE: 1999-11-03
, NUMBER OF SEQ ID NOS: 8564
, SOFTWARE: PatentIn Ver. 3.0
, SEQ ID NO 3252
, LENGTH: 105
, TYPE: DNA
, ORGANISM: Homo sapiens
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (28)..(28)
, OTHER INFORMATION: n equals a,t,g, or c
, NAME/KEY: misc_feature
, LOCATION: (40)..(40)
, OTHER INFORMATION: n equals a,t,g, or c
, NAME/KEY: misc_feature
, LOCATION: (53)..(53)
, OTHER INFORMATION: n equals a,t,g, or c
, NAME/KEY: misc_feature
, LOCATION: (72)..(72)
, OTHER INFORMATION: n equals a,t,g, or c
, NAME/KEY: misc_feature
, LOCATION: (77)..(77)
, OTHER INFORMATION: n equals a,t,g, or c
US-10-106-698-3252

```

Qy 169 GGCAGGG 175  
Db 18 GTCAGAG 12

## RESULT 9

```

US-09-947-274-145/C
; Sequence 145, Application US/09947274
; Publication No. US20030017499A1
; GENERAL INFORMATION:
; APPLICANT: Li, Xiangliang
; TITLE OF INVENTION: METHOD FOR DETECTING TRANSCRIPTION FACTOR-PROTEIN INTERACTIONS
; FILE REFERENCE: 26757-705
; CURRENT APPLICATION NUMBER: US/09/947, 274
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 09/877, 738
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877, 243
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877, 403
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877, 705
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 145
; LENGTH: 78
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hybridization probe MP74
US-09-947-274-145

```

	Query Match	9.48;	Score 23.9;	DB 3;	Length 78;
	Best Local Similarity	59.7;	Pred. No. 2.1e+03;		
	Matches 40;	Conservative 0;	Mismatches 27;	Indels 0;	Gaps 0;
Qy	109	AGTTTCGGGCTCCAGGTTCCGGTGC	CGCCCTTCAGGTTTGAGGCCAGACAGCTCCGAGTCG	168	
Db	78	AGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTCAG	19		
Qy	169	GGCAGGG	175		
Db	18	GTCCAGAG	12		

PRECIPITATION

```

RESULI 10
US-09-877-738A-145/c
; Sequence 145, Application US/09877738A
; Publication No. US2003022173A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED
; TITLE OF INVENTION: TRANSCRIPTION FACTORS
; FILE REFERENCE: 26757-701
; CURRENT APPLICATION NUMBER: US/09/877, 738A
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 145
; LENGTH: 78
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hybridization probe MP74
US-09-877-738A-145

```

Query Match 9.4%; Score 23.8; DB 3; Length 78;  
Best Local Similarity 59.7%; Pred. No. 2.1e+03;  
Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;  
Qy 109 AGTTTCGGGCTCCAGGTTCCGGTGTCCCTTCAGGTTTGAGGCCAGACAGCTCCAGTCG 168  
Db 78 AGCTTCAGGTCAGAGGTCAGAGACTAGCTTCAGGTTCAGAGGTTCAGAGAGCTAGCTTCAG 19

## RESULT 11

```

US-09-877-403A-145/c
; Sequence 145, Application US/09877403A
; Publication No. US20040214166A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD FOR IDENTIFYING
; TITLE OF INVENTION: ACTIVATED TRANSCRIPTS
; FILE REFERENCE: 26757-703
; CURRENT APPLICATION NUMBER: US/09/877
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 145
; LENGTH: 78
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hybridization probe
US-09-877-403A-145

```

```

Query Match          9.4%; Score 23.8; DB 4; Length 78;
Best Local Similarity 59.7%; Pred. No. 2.1e+03;
Matches 40: Conservative 0; Mismatches 27; Indels 0; Gaps 0

```

Qy 109 AGTTTCCGGCTCCAGGTTTCGGTGTCGCCCTGAGGTTTGAGGCCACAGACAGCTCGCAGTCG 168

Qy 169 GGCAGGG 175  
| | | |  
Db 18 GTCAGAG 12

## RESULT 12

```

US-10-779-595-145/c
; Sequence 145, Application US/10779595
; Publication No. US20040132090A1
; GENERAL INFORMATION:
; APPLICANT: Li, Xianqiang
; TITLE OF INVENTION: METHOD, ARRAY AND
; FILE REFERENCE: 26757-702.301
; CURRENT APPLICATION NUMBER: US/10/77
; CURRENT FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: 09/877,243
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 145
; LENGTH: 78
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hybridization pr
US-10-779-595-145

```

Query Match 9.4%; Score 23.8; DB 8; Length 78;  
Best Local Similarity 59.7%; Pred. No. 2.1e+03;  
Matches 40: Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 109 AGTTTCCGGCTCCAGGTTCCGGTFCGCCCTGAGGTTGAGGCCAGACAGCTCGCAGTCG 168

nb 78 AGTTTCAGTCCAGGCTCAGAGAGTACGTTTCAGTTCAGGTCACAGAGCTCAGAGGTCAGTTTCAG 19

QY 169 GGCAGG 175  
| | | |  
Db 18 GTCAGAG 12



RESULT 13  
US-10-781-499-1  
; Sequence 1, Application US/10781499  
; Publication No. US2005005406A1  
; GENERAL INFORMATION:  
; APPLICANT: Metabolic Explorer  
; TITLE OF INVENTION: Method for the preparation of an evolved microorganism for the ca  
; FILE OF INVENTION: or modification of metabolic pathways  
; FILE REFERENCE: D20701/ 345774  
; CURRENT APPLICATION NUMBER: US/10781.499  
; CURRENT FILING DATE: 2004-02-18  
; PRIOR APPLICATION NUMBER: FR 0301924  
; PRIOR FILING DATE: 2003-02-18  
; PRIOR APPLICATION NUMBER: FR 0305768  
; PRIOR FILING DATE: 2003-05-14  
; PRIOR APPLICATION NUMBER: FR 0305769  
; PRIOR FILING DATE: 2003-05-14  
; PRIOR APPLICATION NUMBER: FR 0313054  
; PRIOR FILING DATE: 2003-11-06  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 100  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: DmetE  
US-10-781-499-1

Query Match 9.3%; Score 23.4; DB 10; Length 100;  
Best Local Similarity 63.2%; Pred. No. 3e+03;  
Matches 36; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 100 CAGGGCTGATTCGGCTCCAGGTCGCGTGTCCGCTGAGGTTGAGGCCAGAC 156  
Db 12 CAAGTTCCGCGCCCTGCACCATGTTCCGACGTGCGCGCGGTTTCTGCGCCAGCC 68

RESULT 14  
US-09-796-692-6323  
; Sequence 6323, Application US/09796692  
; Publication No. US20020198362A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY  
; FILE OF INVENTION: HEMATOLOGICAL MALIGNANCIES  
; FILE REFERENCE: 2077.001200  
; CURRENT APPLICATION NUMBER: US/09796.692  
; CURRENT FILING DATE: 2001-03-01  
; PRIOR APPLICATION NUMBER: 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: 60/223,416  
; PRIOR FILING DATE: 2000-08-04  
; PRIOR APPLICATION NUMBER: 60/223,378  
; PRIOR FILING DATE: 2000-08-07  
; PRIOR APPLICATION NUMBER: US 09/796,692  
; PRIOR FILING DATE: 2001-03-01  
; NUMBER OF SEQ ID NOS: 10467  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6323  
; LENGTH: 120  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-040-862-6323

; PRIOR FILING DATE: 2000-08-04  
; PRIOR APPLICATION NUMBER: 60/223,378  
; PRIOR FILING DATE: 2000-08-07  
; NUMBER OF SEQ ID NOS: 9597  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6323  
; LENGTH: 120  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-796-692-6323

Query Match 9.3%; Score 23.4; DB 3; Length 120;  
Best Local Similarity 60.0%; Pred. No. 3e+03;  
Matches 39; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 141 AGGTTTGGAGCCACAGACATCGCAGTCGGGCGGAGGGCGGGGAGAGACGAGCGGCTC 200  
Db 53 AGGTTTGGATGCAAGATGCTCTGGGAAGTCACGCGCAGATATGGGGGGAGAAAAGCTGCTC 112  
Qy 201 TGGCC 205  
Db 113 AGACC 117

RESULT 15  
US-10-040-862-6323  
; Sequence 6323, Application US/10040862  
; Publication No. US20030078396A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Retter, Marc  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
; FILE OF INVENTION: Hematological Malignancies  
; FILE REFERENCE: 014058-013520US  
; CURRENT APPLICATION NUMBER: US/10/040.862  
; CURRENT FILING DATE: 2001-11-06  
; PRIOR APPLICATION NUMBER: US 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: US 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: US 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: US 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: US 60/223,416  
; PRIOR FILING DATE: 2000-08-04  
; PRIOR APPLICATION NUMBER: US 60/223,378  
; PRIOR FILING DATE: 2000-08-07  
; PRIOR APPLICATION NUMBER: US 09/796,692  
; PRIOR FILING DATE: 2001-03-01  
; NUMBER OF SEQ ID NOS: 10467  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6323  
; LENGTH: 120  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-040-862-6323

Query Match 9.3%; Score 23.4; DB 6; Length 120;  
Best Local Similarity 60.0%; Pred. No. 3e+03;  
Matches 39; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
Qy 141 AGGTTTGAGGCCAGACAGCTCGCAGTCGGCGAGGGGGGGGAGAGACGAGCGGCTC 200  
Db 53 AGGTTTGAGTCGAAGATGCTCTGGGAAGTCACGACAGATATGGGGGGGAGAAAGCTGCTC 112  
Qy 201 TGGCC 205  
Db 113 AGACC 117

Search completed: June 19, 2007, 18:07:52  
Job time : 3939 secs

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 13:30:48 ; Search time 12307 Seconds  
(without alignments)  
1270.361 Million cell updates/sec

Title: US-10-604-726A-8797  
Perfect score: 252  
Sequence: 1 99gttatctgcaactgagag.....tctctcttcctgcacacctcc 252

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 1909528

Minimum DB seq length: 0

Maximum DB seq length: 120

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST.\*

- 1: gb\_est1.\*
- 2: gb\_est3.\*
- 3: gb\_est4.\*
- 4: gb\_est5.\*
- 5: gb\_est6.\*
- 6: gb\_est7.\*
- 7: gb\_est8.\*
- 8: gb\_est9.\*
- 9: gb\_est10.\*
- 10: gb\_est11.\*
- 11: gb\_est12.\*
- 12: gb\_est13.\*
- 13: gb\_est14.\*
- 14: gb\_est15.\*
- 15: gb\_gss1.\*
- 16: gb\_gss2.\*
- 17: gb\_gss3.\*
- 18: gb\_gss4.\*
- 19: gb\_gss5.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	11.5	100	15	AZ769498
C 2	28.6	11.3	103	12	EC491510
C 3	28	11.1	97	12	EC465112
4	27.6	11.0	103	17	CG574657
5	27	10.7	110	11	EE366986
6	26.2	10.4	82	17	CG535738
C 7	25.8	10.2	93	11	EC566335
C 8	25.8	10.2	110	9	CK014560
C 9	25.8	10.2	110	17	CL952591
C 10	25.8	10.2	111	12	EB652145
11	25.8	10.2	113	12	EC536793
12	25.6	10.2	99	7	AV841732
13	25.6	10.2	103	18	DU408432
C 14	25.6	10.2	117	17	CG255380

C 15	25.2	10.0	103	7	AW800261
C 16	25.2	10.0	103	12	EC523717
C 17	25.2	10.0	112	5	BY857392
C 18	25	9.9	100	12	DV900899
C 19	25	9.9	108	15	AZ697609
C 20	24.8	9.8	89	2	BG718505
C 21	24.8	9.8	116	16	BZ836170
22	24.8	9.8	120	19	CNS02660
23	24.6	9.8	107	8	CB219192
24	24.6	9.8	109	11	EC547122
25	24.6	9.8	119	16	BZ987003
C 26	24.4	9.7	95	2	BF724320
C 27	24.4	9.7	109	13	DV552589
28	24.4	9.7	119	13	DN773586
29	24.2	9.6	83	12	EC134983
C 30	24.2	9.6	104	9	CN071764
31	24.2	9.6	115	17	CW117487
32	24.2	9.6	117	18	DU188381
33	24	9.5	92	16	BZ585533
34	24	9.5	100	9	CK005996
35	24	9.5	100	17	CL952595
C 36	24	9.5	101	8	CD029354
37	24	9.5	102	16	CC376448
C 38	24	9.5	105	9	CK451897
39	24	9.5	116	8	CF741809
40	23.8	9.4	85	12	EC429664
C 41	23.8	9.4	93	9	CK100624
42	23.8	9.4	101	3	BJ965328
43	23.8	9.4	102	3	BJ965717
44	23.8	9.4	102	3	BJ970068
45	23.8	9.4	103	3	BJ967675

## ALIGNMENTS

RESULT 1  
AZ769498

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AZ769498 100 bp DNA linear GSS 16-FEB-2001  
clone UUGCLM0570K16 F, genomic survey sequence.

AZ769498

AZ769498.1 GI:12889695

GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 100)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von

Niederhauser, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0570 row: K column: 16

Seq primer: GGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 100.

Location/Qualifiers

1..100

/organism="Mus musculus"

FEATURES

source

/mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGCIM0570K16"  
 /sex="male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGCLM library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GII4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 11.5%; Score 29; DB 15; Length 100;  
 Best Local Similarity 71.7%; Pred. No. 3.6e+03;  
 Matches 38; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 147 GAGGCCACAGCTCGCAGTCCGGCAGCGGCGGAGAGCAGCGCGCT 199  
 Db 23 GCGCAGGTGAGCGCTCCGCCGCGGAGAGCGGCGGAGCGCGGCT 75

## RESULT 2

EC491510/c  
 LOCUS EC491510 103 bp mRNA linear EST 22-JUN-2006  
 DEFINITION IT189508 0197\_3386 LNCAP + R1881 synthetic Androgen human prostate library Homo sapiens cDNA similar to  
 ENSG00000197152|ENST00000356485, mRNA sequence.

ACCESSION EC491510 GI:109531102

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 103)

AUTHORS Bainbridge,M.N., Warren,R.L., Hirst,M., Romanuk,T., Zeng,T., Go.A., Delany,A., Griffith,M., Hickenbotham,M., Magrini,V., Mardis,E.R., Sadar,M.D., Siddiqui,A.S., Marra,M.A. and Jones,S.J.M.

TITLE Analysis of the prostate cancer cell line LNCap transcriptome using a sequencing-by-synthesis approach

JOURNAL Unpublished (2006)

COMMENT Contact: Steven Jones

British Columbia Genome Sciences Centre

Email: sjones@bcgsc.ca

EST was generated using 454 life sciences sequence-by-synthesis sequencer.

## FEATURES

source

Location/Qualifiers

1..103

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/sex="male"

/tissue type="prostate"

/cell line="LNCap"

/clone\_lib="LNCAP + R1881 synthetic Androgen human

## prostate library"

/note="LNCap human prostate cancer cells (American Type Culture Collection; Bethesda, MD) were maintained in RPMI-1640 media (StemCell Technologies; Vancouver, BC) supplemented with 10% fetal bovine serum (FBS; StemCell Technologies) and incubated at 37C with 5% CO2. Cells at passage 38 were plated at a density of approximately 4x10^6 cells per T175 flask. Cells were serum-starved for 48 hours prior to treatment for 16 hours with 10 nM R1881 (PerkinElmer; Woodbridge, Canada). Cells were harvested and total RNA was extracted from the cells using TRIzol Reagent (Invitrogen Life Technologies, Carlsbad, CA) following the manufacturer's instructions"

## ORIGIN

Query Match 11.3%; Score 28.6; DB 12; Length 103;  
 Best Local Similarity 57.1%; Pred. No. 4.7e+03;  
 Matches 52; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 39 CCAAGTTGGAAGCGGCTTTCCTGTTTCTGATGAGAGTCTCTGACTCCCTCG 98  
 Db 103 CCCTGTTGGCAGACTGCTTTTTTTTTTTTGTAGACGGAGTCTTGTGCTCG 44

Qy 99 CCACGGCTGAGTTCCGGCTCCAGGTTCCG 129

Db 43 GCTGGAGTGCAGTGGCCTGATCTCGGCTCAC 13

## RESULT 3

EC465112/c

LOCUS EC465112 97 bp mRNA linear EST 21-JUN-2006

DEFINITION 2T010516 3708 0837 LNCAP + R1881 synthetic Androgen human prostate library Homo sapiens cDNA similar to

ENSG00000077235|ENST00000356183, mRNA sequence.

ACCESSION EC465112 GI:109429135

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 97)

AUTHORS Bainbridge,M.N., Warren,R.L., Hirst,M., Romanuk,T., Zeng,T., Go.A., Delany,A., Griffith,M., Hickenbotham,M., Magrini,V., Mardis,E.R., Sadar,M.D., Siddiqui,A.S., Marra,M.A. and Jones,S.J.M.

TITLE Analysis of the prostate cancer cell line LNCap transcriptome using a sequencing-by-synthesis approach

JOURNAL Unpublished (2006)

COMMENT Contact: Steven Jones

British Columbia Genome Sciences Centre

Email: sjones@bcgsc.ca

EST was generated using 454 life sciences sequence-by-synthesis sequencer.

Location/Qualifiers

1..97

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/sex="male"

/tissue type="prostate"

/cell line="LNCap"

/clone\_lib="LNCAP + R1881 synthetic Androgen human

prostate library"

/note="LNCap human prostate cancer cells (American Type Culture Collection; Bethesda, MD) were maintained in RPMI-1640 media (StemCell Technologies; Vancouver, BC) supplemented with 10% fetal bovine serum (FBS; StemCell Technologies) and incubated at 37C with 5% CO2. Cells at passage 38 were plated at a density of approximately 4x10^6 cells per T175 flask. Cells were serum-starved for 48 hours prior to treatment for 16 hours with 10 nM R1881

(PerkinElmer; Woodbridge, Canada). Cells were harvested and total RNA was extracted from the cells using TRIzol Reagent (Invitrogen Life Technologies, Carlsbad, CA) following the manufacturer's instructions"

ORIGIN  
Query Match 11.1%; Score 28; DB 12; Length 97;  
Best Local Similarity 58.3%; Pred. No. 6.9e+03;  
Matches 49; Conservative 0; Mismatches 35; Indels 0; Gaps 0;  
QY 128 GCGTGTGCGCCCTGAGTTTGGAGGCGACACACTCGCAGTCGGCAGGAGGCGGGGAG 187  
DB 88 GTGTGCTTGGAGATCTTGGAGCATATACACGGTGTGGATGACAGAGGAGCTG 29  
QY 188 AGACGAGCGCTCGGCCCTTAA 211  
DB 28 CGACAGACGGTTCTCGGACCTTAA 5

RESULT 4  
CG574657 103 bp mRNA linear GSS 02-OCT-2003  
LOCUS OST207730 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST207730,  
DEFINITION mRNA sequence.  
ACCESSION CG574657  
VERSION CG574657.1 GI:37364994  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 103)  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 103)  
AUTHORS Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,  
Piggott, J., BeltrandeRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,  
Friddie, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,  
Key, B.W., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,  
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,  
Sparkes, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,  
Zhu, Q., Person, C. and Sands, A.T.  
TITLE Wk1 kinase deficiency lowers blood pressure in mice: a gene-trap  
screen to identify potential targets for therapeutic intervention  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
PUBMED 14610273  
COMMENT Contact: Zambrowicz BP  
OmniBank  
Lexicon Genetics Incorporated  
4000 Research Forest Drive, The Woodlands, TX 77381, USA  
Email: materials@lexgen.com  
Gene trap sequence tag generated by 3' RACE from mouse ES cells as  
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)  
Class: Gene Trap.

FEATURES  
Location/Qualifiers  
1..103  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129Sv/Ev"  
/db\_xref="taxon:10090"  
/clone="OST207730"  
/cell\_type="embryonic stem cell"  
/clone\_lib="Mus musculus 129Sv/Ev"

ORIGIN  
Query Match 11.0%; Score 27.6; DB 17; Length 103;  
Best Local Similarity 67.2%; Pred. No. 8.9e+03;  
Matches 39; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 39 CCAAGTTGGAGGCGCTTCTTCTCTCTTCTCGATCGACAGTCCTTGACTCCCTC 96  
DB 42 CCAACTTGATAGACACTTGAGGTTCTTCTTCTCGATCAAGCGTGCTTACTGCTC 99

RESULT 5

EE366986

LOCUS LB02989.CR\_P21 GC\_BGC-29 Bos taurus cDNA clone IMAGE:8486471, mRNA  
DEFINITION sequence.  
ACCESSION EE366986  
VERSION EE366986.1 GI:112227366  
KEYWORDS EST.  
SOURCE Bos taurus (cattle)  
ORGANISM Bos taurus

REFERENCE 1 (bases 1 to 110)  
AUTHORS Moore, S., Alexander, L., Brownstein, M., Guan, L., Lobo, S., Meng, Y.,  
Tanaguchi, M., Wang, Z., Yu, J., Prange, C., Schreiber, K., Shenmen, C.,  
Wagner, L., Bala, M., Barbazuk, S., Barber, S., Babakaliff, R.,  
Beland, J., Chun, E., Del Rio, L., Gibson, S., Hanson, R.,  
Kirkpatrick, R., Liu, J., Matsuo, C., Mayo, M., Santos, R.R., Stott, J.,  
Tsai, M., Wong, D., Siddiqui, A., Holt, R., Jones, S.J. and Marra, M.A.

REFERENCE 1 (bases 1 to 110)  
AUTHORS Moore, S., Alexander, L., Brownstein, M., Guan, L., Lobo, S., Meng, Y.,  
Tanaguchi, M., Wang, Z., Yu, J., Prange, C., Schreiber, K., Shenmen, C.,  
Wagner, L., Bala, M., Barbazuk, S., Barber, S., Babakaliff, R.,  
Beland, J., Chun, E., Del Rio, L., Gibson, S., Hanson, R.,  
Kirkpatrick, R., Liu, J., Matsuo, C., Mayo, M., Santos, R.R., Stott, J.,  
Tsai, M., Wong, D., Siddiqui, A., Holt, R., Jones, S.J. and Marra, M.A.

REFERENCE 1 (bases 1 to 110)  
AUTHORS Moore, S., Alexander, L., Brownstein, M., Guan, L., Lobo, S., Meng, Y.,  
Tanaguchi, M., Wang, Z., Yu, J., Prange, C., Schreiber, K., Shenmen, C.,  
Wagner, L., Bala, M., Barbazuk, S., Barber, S., Babakaliff, R.,  
Beland, J., Chun, E., Del Rio, L., Gibson, S., Hanson, R.,  
Kirkpatrick, R., Liu, J., Matsuo, C., Mayo, M., Santos, R.R., Stott, J.,  
Tsai, M., Wong, D., Siddiqui, A., Holt, R., Jones, S.J. and Marra, M.A.

TITLE Bovine Genome Sequencing Program: Full-length cDNA Sequencing  
JOURNAL Unpublished (2005)  
COMMENT Contact: Robert Kirkpatrick  
Canada's Michael Smith Genome Sciences Centre  
BC Cancer Agency  
Suite 100, 570 West 7th Avenue, Vancouver, British Columbia,  
Canada, V5Z 4S6  
Tel: 1-604-707-5900 x5406  
Fax: 1-604-876-3561  
Email: robertk@bcgsc.ca  
Plate: LB02989 row: P column: 21  
High quality sequence stop: 110.

FEATURES  
source  
1..110  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/strain="Li Hereford"  
/db\_xref="taxon:9913"  
/clone="IMAGE:8486471"  
/sex="male"  
/tissue type="Skin"  
/dev\_stage="6 months old fetus"  
/lab\_host="E. coli DH10B T1 Phage resistant"  
/clone\_lib="GC BGC-29"  
/note="Vector: pExpress 1; Site 1: Blunt (5' end of cDNA);  
Site 2: NotI (3' end of cDNA)"

ORIGIN  
Query Match 10.7%; Score 27; DB 11; Length 110;  
Best Local Similarity 54.5%; Pred. No. 1.3e+04;  
Matches 54; Conservative 0; Mismatches 45; Indels 0; Gaps 0;  
QY 92 CCCTCTGCGCGCTGAGTTTCCGGCTCCAGTTCCGGTTCGGCTGCGCTGAGTTTCAGGC 151  
DB 9 CGCTGACCGCTGGGGGAAGCCCGGAGCCCGCAAGTCCCTTCCTCTCTCTTGGACC 68  
QY 152 CAGACAGCTCCGAGTCGGGCGAGGAGGCGGGGAGAGA 190  
DB 69 CTGACTGGAGCGCGGCGGCTGGGTGGGGGGGTAGGGA 107

RESULT 6  
CG535738  
LOCUS OST122945 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST122945,  
DEFINITION mRNA sequence.  
ACCESSION CG535738  
VERSION CG535738.1 GI:37322310  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 110)  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 110)  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 110)  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 110)  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 110)  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 110)  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 110)  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 110)  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /sex="male"  
 /tissue\_type="prostate"  
 /cell\_line="LNCap"  
 /clone\_lib="LNCAP + R1881 synthetic Androgen human prostate library"  
 /notes="LNCap human prostate cancer cells (American Type Culture Collection; Bethesda, MD) were maintained in RPMI-1640 media (StemCell Technologies; Vancouver, BC) supplemented with 10% fetal bovine serum (FBS; StemCell Technologies) and incubated at 37C with 5% CO2. Cells at passage 38 were plated at a density of approximately 4x10^6 cells per T175 flask. Cells were serum-starved for 48 hours prior to treatment for 16 hours with 10 nM R1881 (perkinElmer; Woodbridge, Canada). Cells were harvested and total RNA was extracted from the cells using TRIzol Reagent (Invitrogen Life Technologies, Carlsbad, CA) following the manufacturer's instructions"

ORIGIN	Query Match	10.2%;	Score 25.8;	DB 11;	Length 93;
Best Local Similarity	58.4%;		Pred. No. 2.8e+04;		
Matches	45;	Conservative	0;	Mismatches 32;	Indels 0; Gaps 0;

Qy	66	TTTCTGTGGATGCAGAGTCCTCTCACTCCCTCTCCACGGCGTGA	TTTCGGCTCCAGGT	125
Db	85	TTGCCTGGCTGCTCTCTCTCTTCTGAGAGCTGTTCACCGCTGCTCTTCGGTTGGAGGC	26	
Qy	126	TCGGGTCTGCCCTGAG	142	
Db	25	TCTCATGCTCTTTGGG	9	

RESULT 8  
 CK014560/c  
 LOCUS  
 DEFINITION  
 library Oryza sativa (indica cultivar-group) cDNA 5', mRNA  
 EST.  
 CK014560  
 CK014560.1 GI:58604032  
 Oryza sativa (indica cultivar-group)  
 Oryza sativa (indica cultivar-group)  
 Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 110)  
 Yu, J., Wang, J., Lin, W., Li, S., Li, H., Zhou, J., Ni, P., Dong, W., Hu, S., Zeng, C., Zhang, J., Zhang, Y., Li, R., Xu, Z., Li, S., Li, X., Zheng, H., Cong, L., Lin, L., Yan, J., Geng, J., Li, G., Shi, J., Liu, J., Lv, H., Li, J., Wang, J., Deng, X., Ran, L., Shi, X., Wang, X., Wu, Q., Li, C., Ren, X., Wang, J., Wang, X., Li, D., Liu, D., Zhang, X., Ji, Z., Zhao, W., Sun, Y., Zhang, Z., Bao, J., Han, Y., Dong, L., Ji, J., Chen, P., Wu, S. and Liu, J.  
 The Genomes of Oryza sativa: A History of Duplications  
 PLoS Biol. 3 (2), e38 (2005)  
 15685292  
 Contact: Yan Zhou  
 Bioinformatics Department  
 Hangzhou Genomics Institute  
 No.51 Zhijiang Road, Hangzhou 310008, China  
 Tel: 86-571-56805886  
 Fax: 86-571-56805884  
 Email: zhouyan@genomics.org.cn  
 Seq primer: M13 Forward  
 High quality sequence stop: 110  
 POLYA-No.  
 Location/Qualifiers  
 1..110  
 /organism="Oryza sativa (indica cultivar-group)"

FEATURES  
 source

```

FEATURES
location/Qualifiers
1. .110
/organism="Oryza sativa (indica cultivar-group)"

```

```

/mol type="mRNA"
/cultivar="PA64s"
/db_xref="taxon:39946"
/tissue type="panicle"
/cell type="sterile"
/dev stage="heading/flowering"
/clone_lib="Oryza sativa cv. PA64s panicle sterile cDNA
library"

ORIGIN
Query Match      10.2%; Score 25.8; DB 9; Length 110;
Best Local Similarity 60.9%; Pred. No. 2.8e+04;
Matches 42; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 127 CGCGTGTGCGCCTTGGAGTTTGAGCCACAGAGTCGCGAGTGGGAGGGGGGGA 186
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 77 CGCAGCGCGCCTTCAGCTTGAGGCGCCACATGCGCGCGCGGAGATGGGGGGA 18

Qy 187 GAGACGAGC 195
      ||||| |||||
Db 17 GAGAGAGC 9

RESULT 9
CL952591/c
LOCUS      CL952591      110 bp      DNA      linear      GSS 21-SEP-2004
DEFINITION OsrIRUA001748 Oryza sativa Express Library Oryza sativa (indica
cultivar-group) genomic, genomic survey sequence.
ACCESSION  CL952591
VERSION     CL952591
SOURCE      CL952591.1 GI:52364600
ORGANISM    Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzoideae; Oryza.
REFERENCE   1 (bases 1 to 110)
AUTHORS    Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
Wong, G.K.S., Deng, X.W. and Wang, J.
TITLE      An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
JOURNAL    Unpublished (2004)
COMMENT    Contact: Chen Chen
            Department of Bioinformatic
            Beijing Institute of Genomics
            Chinese Academy of Sciences, Beijing 101300, China
            Tel: 86-10-80481559
            Fax: 86-10-80488676
            Email: chenchen@genomics.org.cn
            Rice genomic sequence.
            Class: exon-trapped.
FEATURES    Location/Qualifiers
             source
               1..110
               /organism="Oryza sativa (indica cultivar-group)"
               /mol_type="genomic DNA"
               /db_xref="taxon:39946"
               /clone_lib="Oryza sativa Express Library"
               /notes="Oryza sativa exon trapped genomic sequences"

ORIGIN
Query Match      10.2%; Score 25.8; DB 17; Length 110;
Best Local Similarity 60.9%; Pred. No. 2.8e+04;
Matches 42; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 127 CGCGTGTGCGCCTTGGAGTTTGAGCCACAGAGTCGCGAGTGGGAGGGGGGGA 186
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 77 CGCAGCGCGCCTTCAGCTTGAGGCGCCACATGCGCGCGCGGAGATGGGGGGA 18

Qy 187 GAGACGAGC 195
      ||||| |||||
Db 17 GAGAGAGC 9

/mol type="mRNA"
/db_xref="taxon:39946"
/tissue type="panicle"
/cell type="sterile"
/dev stage="heading/flowering"
/clone_lib="Oryza sativa cv. PA64s panicle sterile cDNA
library"

ORIGIN
Query Match      10.2%; Score 25.8; DB 9; Length 110;
Best Local Similarity 60.9%; Pred. No. 2.8e+04;
Matches 42; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 127 CGCGTGTGCGCCTTGGAGTTTGAGCCACAGAGTCGCGAGTGGGAGGGGGGGA 186
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 77 CGCAGCGCGCCTTCAGCTTGAGGCGCCACATGCGCGCGCGGAGATGGGGGGA 18

Qy 187 GAGACGAGC 195
      ||||| |||||
Db 17 GAGAGAGC 9

RESULT 10
EB652145/c
LOCUS      EB652145      111 bp      mRNA      linear      EST 25-APR-2006
DEFINITION GmUSCLMBHI03pTriplex214j07f1 Gillichthys mixed tissue (liver,
muscle, brain, heart, intestine) library 2 Gillichthys mirabilis
cDNA clone 14j07 5', mRNA sequence.
ACCESSION  EB652145
VERSION     EB652145
SOURCE      EB652145.1 GI:93277671
ORGANISM    Gillichthys mirabilis (long-jawed mudsucker)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorphi; Acanthopterygii; Percomorpha; Perciformes;
Gobioidi; Gobiidae; Gillichthys.
REFERENCE   1 (bases 1 to 111)
AUTHORS    Gracey, A.Y.
TITLE      Unpublished, Andrew Y. Gracey
JOURNAL    Unpublished (2006)
COMMENT    Contact: Andrew Y. Gracey
            Biological Sciences
            University of Southern California
            3616 Trousdale Parkway #107, Mail Code 0371, Los Angeles, CA 90089,
            USA
            Tel: 213-740-2288
            Fax: 213-740-8123
            Email: gracey@usc.edu
            Vector has been trimmed from this EST.
            Plate: 14 row: j column: 07
            Seq primer: Triplex 5' LD (5'-CTCGGAGGCGCCATTGTGGT-3')
            High quality sequence stop: 111.
            Location/Qualifiers
             source
               1..111
               /organism="Gillichthys mirabilis"
               /mol_type="mRNA"
               /db_xref="taxon:8222"
               /clone="14j07"
               /sex="Male & female"
               /tissue type="Liver, muscle, brain, heart, intestine"
               /dev_stage="Adult"
               /lab_host="E.coli Electromax DH10B"
               /clone_lib="Gillichthys mixed tissue (liver, muscle,
               brain, heart, intestine) library 2"
               /note="Vector: pTriplex2; Site 1: Sfil GGCCATTACGGCC;
               Site 2: Sfil GGCGCTTCGGCC; Normalized and serially
               subcloned cDNA library prepared from environmentally
               challenged animals"

ORIGIN
Query Match      10.2%; Score 25.8; DB 12; Length 111;
Best Local Similarity 56.5%; Pred. No. 2.8e+04;
Matches 48; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy 137 CCTGAGGTTTCAGGCGCAGACAGCTCGAGTCGGGCGGAGGAGAGAGAGCGG 196
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 107 CCTGCTTCTGATCCACATCTGCTGGAAGTGGGCGAGAGCGCAGGATGGATGATG 48

Qy 197 GCTTCGGCCCTTAAATGTTACTTCG 221
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 47 AGTCTGGCCCATCCATCTGTCGGCG 23

RESULT 11
EC536793
LOCUS      EC536793      113 bp      mRNA      linear      EST 22-JUN-2006
DEFINITION 17264505.0517 1775 LNCAP + R1881 synthetic Androgen human prostate
library Homo sapiens cDNA similar to
ENSG00000176095|ENST00000321599, mRNA sequence.
ACCESSION  EC536793
VERSION     EC536793
SOURCE      EC536793.1 GI:109576387
            Homo sapiens (human)

```

ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Homo sapiens		Bainbridge M.N., Warren R.L., Hirst M., Romanuk T., Zeng T., Go A., Delany A., Griffith M., Hickenbotham M., Magrini V., Madis E.R., Sadar M.D., Siddiqui A.S., Marra M.A. and Jones S.J.M.	Analysis of the prostate cancer cell line LNCap transcriptome using a sequencing-by-synthesis approach	Unpublished (2006)	Contact: Steven Jones
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.	1 (bases 1 to 113)				Bioinformatics
					British Columbia Genome Sciences Centre
					Email: sjones@bcgsc.ca
					EST was generated using 454 life sciences sequence-by-synthesis sequencer.

```

sequence:      Location/Qualifiers
1. .113
   /organism="Homo sapiens"
   /mol_type="mRNA"
   /db_xref="taxon:9606"
   /sex="male"
   /tissue_type="prostate"
   /cell_line="LNCaP"
   /clone_lib="LNCAP + R1881 synthetic Androgen human
   prostate library"
   /notes="LNCaP human prostate cancer cells (American Type
   Culture Collection; Bethesda, MD) were maintained in
   RPMI-1640 media (StemCell Technologies; Vancouver, BC)
   supplemented with 10% fetal bovine serum (FBS; StemCell
   Technologies) and incubated at 37C with 5% CO2. Cells at
   passage 38 were plated at a density of approximately
   4x10^6 cells per T175 flask. Cells were serum-starved for
   48 hours prior to treatment for 16 hours with 10 nM R1881
   (perkinElmer; Woodbridge, Canada). Cells were harvested
   and total RNA was extracted from the cells using TRIzol
   Reagent (Invitrogen Life Technologies, Carlsbad, CA)
   following the manufacturer's instructions"

```

ORIGIN					
	Query Match	10.2%	Score 25.8;	DB 12;	Length 113;
	Best Local Similarity	58.4%;	Pred. No. 2.8e+04;		
	Matches	45;	Conservative	0;	Mismatches 32; Indels 0; Gaps 0;
<hr/>					
Qy	7	TCTGCAACTGAGAGGGCGTGGTTAAGCGTCCCAAGTTGGAAAGGCGCTTGTCTGT	66		
Dd	17	TCITTTTGCTTCGGGGAACGTGAAGCCCTCGGTTCTGGGAATCCTCTCTGTGTCTCT	76		
<hr/>					
Qy	67	TTTCTGGATGCAGATC	83		
<hr/>					
Dd	77	TTCTGGAAGCTAAGCC	93		

RESULT 12	AV841732	AV841732	LOCUS	DEFINITION	AV841732	Nori Satoh unpublished cDNA library, egg Ciona intestinalis cDNA clone rcieg05m22, mRNA sequence.	99 bp	mrna	linear	EST 07-NOV-2001
ACCESSION	AV841732	AV841732	VERSION	AV841732.1	GI:16785883	EST..	Ciona intestinalis	Ciona intestinalis	Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.	
KEYWORDS			SOURCE			1 (bases 1 to 99)	Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.	Expressed genes in Ciona intestinalis	Unpublished (2000)	Contact: Nori Satoh
ORGANISM							Department of Zoology			Kyoto University

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
Tel: 81-75-753-4081  
Fax: 81-75-705-1113  
Email: sato@ascidian.zool.kyoto-u.ac.jp.

FEATURES  
    source Location/Qualifiers  
        1..99  
            /organism="Ciona intestinalis"  
            /mol\_type="mRNA"  
            /db\_xref="taxon:7719"  
            /clone="rcieg05m22"  
            /tissue type="whole animal"  
            /dev\_stage="egg"  
            /clone\_lib="Nori Satoh unpublished cDNA library, egg"

ORIGIN

Query Match 10.2%; Score 25.6; DB 7; Length 99;  
Best Local Similarity 66.1%; Pred. No. 3.2e+04;  
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
0;

Qy 8 CTCGAAC TAGAGGGCGTGTGAAGCGGTCCCAAGTTGGAAGGGCGCTTTGCTTC 63  
Db 16 CTTTCGTCTAAGTGGGGTTGAATGGGGTTTCCACATTTGAGGGTGACTTTGCTTC 71

RESULT 13	DU408432	DU408432	103 bp	DNA	linear	GSS 05-OCT-2005
LOCUS	1098474026684	CHORI-243	Ovis aries	genomic clone	CH243-202P18,	
DEFINITION	genomic survey sequence.					
ACCESSION	DU408432					
VERSION	DU408432.1	GI:77138562				
KEYWORDS	GSS.					
SOURCE	Ovis aries (sheep)					
ORGANISM	Ovis aries					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;					
	Pecora; Bovidae; Caprinae; Ovis.					
	1 (bases 1 to 103)					
REFERENCE	Kirkness, E., Shetty, J., de Jong, P., McEwan, J. C., Oddy, H. and					
AUTHORS	Cockett, N.					

TITLE  
Ovine BAC End Sequences from Library CHORI-243  
Unpublished (2004)  
Other GSSs: 1098474028028  
Contact: Ewen Kirkness  
The Institute for Genomic Research (TIGR; [www.tigr.org](http://www.tigr.org))  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-795-7536  
Email: [ekirknes@tigr.org](mailto:ekirknes@tigr.org)  
Sequences generated at the J. Craig Venter Institute Joint  
Technology Center (JCVJTC; <http://www.venterinsstitute.org/>).  
Original Trace: 1098474028684 Trace T1: [gnl@t1.g18952333](mailto:gnl@t1.g18952333)  
Insert Length: 184000 Std Error: 0.00 row: P column: 18  
Seq primer: SP6  
Class: BAC ends.

```

Class: BAC ends.
Location/Qualifiers
1. 103
/organism="Ovis aries"
/mol_type="genomic DNA"
/strain="Texel breed"
/db_xref="taxon:9940"
/clone="CH243-202p18"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-243"
/note=vector; pTARGAC2.1; Site 1: EcoRI; Site 2: EcoRI;
The CHORI-243 sheep (M) (Ovis aries) BAC library produced
by Pieter de Jong's lab at CHORI
http://bacpac.chori.org/library.php?id=162"

```

Query Match	10.2%	Score	25.6	DB	18	Length	103
Best Local Similarity	55.7%	Pred. NO.	3.2e+04				
Matches	49	Conservative	0	Mismatches	39	Indels	0
						Gaps	0



Qy 64 TGTTTCTGGATGAGAGTCTCTGACTCCCTCTGCCACGGGCTGAGTTTCCGGCTCCAG 123  
 |||||  
 Db 4 TGTGTTCAAAATGAGAAATCAGAAATGTCACATTTCCAGCTCTGGGTGACGGGGCCGG 63  
 |||||  
 Qy 124 GTTCGCGTGTGCGCCCTGAGGTTTGAGGC 151  
 |||||  
 Db 64 GGTGGGGGGGAGGCTGGGGGTGAGGC 91  
 |||||

RESULT 14  
 CG255380/c  
 LOCUS CG255380 117 bp DNA linear GSS 25-AUG-2003  
 DEFINITION OGVC9292TH\_ZM\_0.7\_1.5\_KB\_Zea\_mays\_genomic\_clone\_ZMMBMA0505P16,  
 genomic survey sequence.

ACCESSION CG255380

VERSION CG255380.1 GI:34159750

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE 1 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.

AUTHORS 1 (bases 1 to 117)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,  
 Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,  
 Citek,R.W., Nurnberg,A., Robbins,D. and Lakey,N.

TITLE Consortium for Maize Genomics

JOURNAL Unpublished (2002)

COMMENT Contact: Cathy Whitelaw

TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TR

Class: methylation filtered.

Location/Qualifiers

1. 117

/organism="Zea mays"

/mol\_type="genomic DNA"

/strain="B73"

/db\_xref="taxon:4577"

/clone="ZMMBMA0505P16"

/clone\_lib="ZM 0.7 1.5 KB"

/notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb

methylation filtered genomic DNA library"

ORIGIN

Query Match 10.2%; Score 25.6; DB 17; Length 117;  
 Best Local Similarity 57.5%; Pred. No. 3.2e+04;  
 Matches 46; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 128 GCGTGTGCGCCCTGAGTTTGAGGCCACAGCTCGCAGTCGGCAGGAGGGGGGAG 187  
 |||||  
 Db 104 GCGGTGCGGGCAGCGATGTGAAGCACGGCGGACATCTCGTGGGGGGGGCGCCAG 45  
 |||||

Qy 188 AGACGAGCGGCTCGGCC 207  
 |||||

Db 44 CGATGTGAAGCTCCGGCCTC 25  
 |||||

RESULT 15  
 AW800261/c  
 LOCUS AW800261 103 bp mRNA linear EST 16-MAY-2000  
 DEFINITION MR2-UM0060-170400-203-e06 UM0060 Homo sapiens cDNA, mRNA sequence.

ACCESSION AW800261

VERSION AW800261.1 GI:7852131

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;

Catarrhini; Hominidae; Homo.

1 (bases 1 to 103)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.,  
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,  
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

10737800

JOURNAL

PUBMED

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=et2=MR2-UM0060-170

400-203-e06&t3=2000-04-17&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 9

High quality sequence stop: 80.

FEATURES

Location/Qualifiers

1. 103

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/dev\_stage="Adult"

/clone\_lib="UM0060"

/note="Organ: uterus; Vector: puc18; Site 1: SmaI; Site 2:

SmaI; A mini-library was made by cloning products derived

from ORESTES PCR (U.S. Letters Patent application No.

196,716 - Ludwig Institute for Cancer Research) profiles

into the pUC 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

ORIGIN

Query Match 10.0%; Score 25.2; DB 7; Length 103;  
 Best Local Similarity 55.8%; Pred. No. 4.1e+04;  
 Matches 48; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 149 GGCACAGAGCTCGCAGTCGGGCGAGGGGGGGGAGACGAGCGGCTCTGGCCCT 208  
 |||||  
 Db 90 GGCACACAACTCGCACTCGGTGAGCTGAGGGTGAAGGGGAGTGCCACAGACATC 31  
 |||||

Qy 209 TAATTGTACTTCGGGCTCGTATTGTC 234  
 |||||

Db 30 CTTCTATAGCCAGGTAACTTTTGTG 5  
 |||||

Search completed: June 19, 2007, 17:02:10

Job time : 12312 secs

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic : nucleic search, using sw model

Run on: June 19, 2007, 13:59:45 ; Search time 2184 Seconds  
(without alignments)  
2500.230 Million cell updates/sec

Title: US-10-604-726A-5135  
Perfect score: 79  
Sequence: 1 ggaaggcggggagagacga.....ucucuccuucgccaccucc 79

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Capext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 3761712

Minimum DB seq length: 0  
Maximum DB seq length: 80

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*

1: gb\_env:\*  
2: gb\_pat:\*  
3: gb\_ph:\*  
4: gb\_pl:\*  
5: gb\_pr:\*  
6: gb\_ro:\*  
7: gb\_sts:\*  
8: gb\_sy:\*  
9: gb\_un:\*  
10: gb\_vi:\*  
11: gb\_ov:\*  
12: gb\_hg:\*  
13: gb\_in:\*  
14: gb\_om:\*  
15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20.2	25.6	49	2	AX772410 Sequence
C 2	19.8	25.1	63	2	E08253 linker. 11/
C 3	19.2	24.3	51	2	AX898740 Sequence
C 4	19.2	24.3	51	2	BD034273 Sequence
C 5	19.2	24.3	51	2	AR734534 Sequence
6	19	24.1	65	2	E08252 linker. 11/
C 7	19	24.1	65	2	AX184576 Sequence
8	18.8	23.8	39	2	A86879 Sequence 19
9	18.8	23.8	39	2	BD070385 Factor X-
10	18.8	23.8	39	2	AR340859 Sequence
C 11	18.8	23.8	54	2	AR118827 Sequence
C 12	18.8	23.8	72	2	CS254876 Sequence
C 13	18.8	23.8	79	2	AR126073 Sequence
C 14	18.6	23.5	55	2	BD270121 Method of
C 15	18.6	23.5	65	2	BD464871 OLIGONUCL
C 16	18.6	23.5	65	2	CQ534358 Sequence
C 17	18.6	23.5	69	6	MMTRB138 X14934 Mouse mRNA
C 18	18.6	23.5	74	5	M18023 Human DNA t

19	18.4	23.3	62	2	AR166135 Sequence
20	18.4	23.3	62	2	AR235763 Sequence
21	18.4	23.3	62	2	AR236505 Sequence
22	18.4	23.3	62	2	AR279563 Sequence
23	18.4	23.3	65	2	AX899943 Sequence
24	18.4	23.3	65	2	BD035476 Sequence
25	18.4	23.3	65	2	AR735737 Sequence
26	18.4	23.3	80	2	BD411059 An Oligon
C 27	18.2	23.0	60	2	BD471330 OLIGONUCL
C 28	18.2	23.0	60	2	CQ540817 Sequence
29	18.2	23.0	65	2	A30344 Artificial
C 30	18.2	23.0	65	2	A30345 Artificial
31	18.2	23.0	65	2	BD461809 OLIGONUCL
32	18.2	23.0	65	2	CQ531296 Sequence
33	18.2	23.0	65	2	I11576 Sequence 28
C 34	18	22.8	40	2	BD298221 Apoptin r
C 35	18	22.8	40	2	AX092132 Sequence
C 36	18	22.8	40	2	AX138312 Sequence
C 37	18	22.8	42	2	AR241798 Sequence
C 38	18	22.8	50	2	CQ004542 Sequence
C 39	18	22.8	51	2	CQ002150 Sequence
C 40	18	22.8	51	2	CQ003187 Sequence
C 41	18	22.8	54	2	CQ861200 Sequence
C 42	18	22.8	78	2	AR031577 Sequence
C 43	18	22.8	78	2	AR065689 Sequence
C 44	18	22.8	78	2	AR097448 Sequence
C 45	18	22.8	78	2	I49966 Sequence 16

## ALIGNMENTS

RESULT 1	AX772410	Sequence 200 from Patent WO03042407.	49 bp	DNA	linear	PAT 02-JUL-2003
LOCUS	AX772410					
DEFINITION	AX772410					
ACCESSION	AX772410.1	GI:32438983				
VERSION	AX772410.1	GI:32438983				
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
FEATURES						
source						
ORIGIN						
Query Match						
Best Local Similarity						
Matches						
Qy						
Db						
RESULT 2						
LOCUS						
DEFINITION						
ACCESSION						
VERSION						
KEYWORDS						

```

SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS
OC
PN
PD
PF
PR
DOI
OGUCHI
PC
C12P21/02,
PC
C12N1/21,C12R1:19),(C12P21/02,C12R1:91);
CC
CC
CC
FH
FH
FT
FT
FEATURES
source
ORIGIN
Query Match
Best Local Similarity
Matches
QY
Db
RESULT 3
AX898740/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
ORIGIN
Query Match
Best Local Similarity
Matches
QY
Db
RESULT 4
BD034273/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS
PN
PD
PF
PR
PI
PC
C12N1/19,C12N1/21,C12N1/15,C12N1/18,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10,
PC
C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC
G06F15/40
CC
FH
FEATURES
source
ORIGIN
Query Match
Best Local Similarity
Matches
QY
Db
RESULT 5
AR734534/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
ORIGIN
Query Match
Best Local Similarity
Matches
QY
Db

```

[illegible][illegible]

/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 24.1%; Score 19; DB 2; Length 65;  
Best Local Similarity 37.3%; Pred. No. 7.2e+04;  
Matches 15; Conservative 10; Mismatches 15; Indels 0; Gaps 0

QY 40 UGUACUUGCGGCUUAUUGUCUCUCCUUCGCAUCC 79  
DB 44 TTTCTTCGTGTCNTCGAANANTCTTCTTCCTTCGCTNNCGCC 5

RESULT 8  
LOCUS A86879 39 bp DNA linear PAT 22-JAN-2001  
DEFINITION Sequence 19 from Patent WO9838317.  
ACCESSION A86879  
VERSION A86879.1 GI:6735670  
KEYWORDS unclassified sequences.  
SOURCE unclassified sequences.  
ORGANISM unclassified sequences.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS Himmelsbach,M. and Eibl,J.  
TITLE FACTOR X ANALOGUES WITH A MODIFIED PROTEASE CLEAVAGE SITE  
JOURNAL Patent: WO 9838317-A 19 03-SEP-1998;  
FEATURES HIMMELSPACH MICHELE (AT); EIBL JOHANN (AT)  
source Location/Qualifiers  
1..39  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

ORIGIN

Query Match 23.8%; Score 18.8; DB 2; Length 39;  
Best Local Similarity 44.7%; Pred. No. 7.9e+04;  
Matches 17; Conservative 9; Mismatches 12; Indels 0; Gaps 0

QY 33 CCUUAUUGUACUUGCGGCUUAUUGUCUCUCCUUC 70  
DB 2 CCAGAATCGATTCTCGTGCTGCTGCTGCTGCTC 39

RESULT 9  
LOCUS BD070385 39 bp DNA linear PAT 27-AUG-2001  
DEFINITION Factor X-analogues with modified protease cleavage site.  
ACCESSION BD070385  
VERSION BD070385.1 GI:22615988  
KEYWORDS JP 2001513631-A/19.  
SOURCE unclassified sequences.  
ORGANISM unclassified sequences.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS Himmelsbach,M., Schlokot,U., Dornier,F., Andreas, Fisch and Eibl,J.  
TITLE Factor X-analogues with modified protease cleavage site  
JOURNAL Patent: JP 2001513631-A 19 04-SEP-2001;  
COMMENT BAXTER AG  
OS Unidentified  
PN JP 2001513631-A/19  
PD 04-SEP-2001  
PF 27-FEB-1998 JP 1998537062  
PR 27-FEB-1997 AT A 335/97  
PI MICHELE HIMMELSPACH,UWE SCHLOKOT,FRIEDRICH DORNIER,ANDREAS PI FISCH,JOHANN EIBL  
PC C12N15/57,C12N9/64,A61K38/48  
CC Strandedness: Single;  
CC Topology: Linear;  
CC Factor X-analogues with modified protease cleavage site FH  
Key Location/Qualifiers  
1..39  
FT source

1 GGAGGGGGGAGAGAGCGGCUUCGCCUUAUU 40  
47 GGCGCGCGCGCGAGCGGCTCAGCGCCCTGCAGT 8

ORIGIN

Query Match 24.1%; Score 19; DB 2; Length 65;  
Best Local Similarity 37.3%; Pred. No. 7.2e+04;  
Matches 15; Conservative 10; Mismatches 15; Indels 0; Gaps 0

QY 40 UGUACUUGCGGCUUAUUGUCUCUCCUUCGCAUCC 79  
DB 44 TTTCTTCGTGTCNTCGAANANTCTTCTTCCTTCGCTNNCGCC 5

RESULT 8  
LOCUS A86879 39 bp DNA linear PAT 22-JAN-2001  
DEFINITION Sequence 19 from Patent WO9838317.  
ACCESSION A86879  
VERSION A86879.1 GI:6735670  
KEYWORDS unclassified sequences.  
SOURCE unclassified sequences.  
ORGANISM unclassified sequences.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS Himmelsbach,M. and Eibl,J.  
TITLE FACTOR X ANALOGUES WITH A MODIFIED PROTEASE CLEAVAGE SITE  
JOURNAL Patent: WO 9838317-A 19 03-SEP-1998;  
FEATURES HIMMELSPACH MICHELE (AT); EIBL JOHANN (AT)  
source Location/Qualifiers  
1..39  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

ORIGIN

Query Match 23.8%; Score 18.8; DB 2; Length 39;  
Best Local Similarity 44.7%; Pred. No. 7.9e+04;  
Matches 17; Conservative 9; Mismatches 12; Indels 0; Gaps 0

QY 33 CCUUAUUGUACUUGCGGCUUAUUGUCUCUCCUUC 70  
DB 2 CCAGAATCGATTCTCGTGCTGCTGCTGCTGCTC 39

RESULT 9  
LOCUS BD070385 39 bp DNA linear PAT 27-AUG-2001  
DEFINITION Factor X-analogues with modified protease cleavage site.  
ACCESSION BD070385  
VERSION BD070385.1 GI:22615988  
KEYWORDS JP 2001513631-A/19.  
SOURCE unclassified sequences.  
ORGANISM unclassified sequences.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS Himmelsbach,M., Schlokot,U., Dornier,F., Andreas, Fisch and Eibl,J.  
TITLE Factor X-analogues with modified protease cleavage site  
JOURNAL Patent: JP 2001513631-A 19 04-SEP-2001;  
COMMENT BAXTER AG  
OS Unidentified  
PN JP 2001513631-A/19  
PD 04-SEP-2001  
PF 27-FEB-1998 JP 1998537062  
PR 27-FEB-1997 AT A 335/97  
PI MICHELE HIMMELSPACH,UWE SCHLOKOT,FRIEDRICH DORNIER,ANDREAS PI FISCH,JOHANN EIBL  
PC C12N15/57,C12N9/64,A61K38/48  
CC Strandedness: Single;  
CC Topology: Linear;  
CC Factor X-analogues with modified protease cleavage site FH  
Key Location/Qualifiers  
1..39  
FT source

1 GGAGGGGGGAGAGAGCGGCUUCGCCUUAUU 40  
47 GGCGCGCGCGCGAGCGGCTCAGCGCCCTGCAGT 8

ORIGIN

Query Match 24.1%; Score 19; DB 2; Length 65;  
Best Local Similarity 37.3%; Pred. No. 7.2e+04;  
Matches 15; Conservative 10; Mismatches 15; Indels 0; Gaps 0

QY 40 UGUACUUGCGGCUUAUUGUCUCUCCUUCGCAUCC 79  
DB 44 TTTCTTCGTGTCNTCGAANANTCTTCTTCCTTCGCTNNCGCC 5

RESULT 8  
LOCUS A86879 39 bp DNA linear PAT 22-JAN-2001  
DEFINITION Sequence 19 from Patent WO9838317.  
ACCESSION A86879  
VERSION A86879.1 GI:6735670  
KEYWORDS unclassified sequences.  
SOURCE unclassified sequences.  
ORGANISM unclassified sequences.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS Himmelsbach,M. and Eibl,J.  
TITLE FACTOR X ANALOGUES WITH A MODIFIED PROTEASE CLEAVAGE SITE  
JOURNAL Patent: WO 9838317-A 19 03-SEP-1998;  
FEATURES HIMMELSPACH MICHELE (AT); EIBL JOHANN (AT)  
source Location/Qualifiers  
1..39  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

ORIGIN

Query Match 23.8%; Score 18.8; DB 2; Length 39;  
Best Local Similarity 44.7%; Pred. No. 7.9e+04;  
Matches 17; Conservative 9; Mismatches 12; Indels 0; Gaps 0

QY 33 CCUUAUUGUACUUGCGGCUUAUUGUCUCUCCUUC 70  
DB 2 CCAGAATCGATTCTCGTGCTGCTGCTGCTGCTC 39

RESULT 9  
LOCUS BD070385 39 bp DNA linear PAT 27-AUG-2001  
DEFINITION Factor X-analogues with modified protease cleavage site.  
ACCESSION BD070385  
VERSION BD070385.1 GI:22615988  
KEYWORDS JP 2001513631-A/19.  
SOURCE unclassified sequences.  
ORGANISM unclassified sequences.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS Himmelsbach,M., Schlokot,U., Dornier,F., Andreas, Fisch and Eibl,J.  
TITLE Factor X-analogues with modified protease cleavage site  
JOURNAL Patent: JP 2001513631-A 19 04-SEP-2001;  
COMMENT BAXTER AG  
OS Unidentified  
PN JP 2001513631-A/19  
PD 04-SEP-2001  
PF 27-FEB-1998 JP 1998537062  
PR 27-FEB-1997 AT A 335/97  
PI MICHELE HIMMELSPACH,UWE SCHLOKOT,FRIEDRICH DORNIER,ANDREAS PI FISCH,JOHANN EIBL  
PC C12N15/57,C12N9/64,A61K38/48  
CC Strandedness: Single;  
CC Topology: Linear;  
CC Factor X-analogues with modified protease cleavage site FH  
Key Location/Qualifiers  
1..39  
FT source

1 GGAGGGGGGAGAGAGCGGCUUCGCCUUAUU 40  
47 GGCGCGCGCGCGAGCGGCTCAGCGCCCTGCAGT 8

ORIGIN

Query Match 24.1%; Score 19; DB 2; Length 65;  
Best Local Similarity 37.3%; Pred. No. 7.2e+04;  
Matches 15; Conservative 10; Mismatches 15; Indels 0; Gaps 0

QY 40 UGUACUUGCGGCUUAUUGUCUCUCCUUCGCAUCC 79  
DB 44 TTTCTTCGTGTCNTCGAANANTCTTCTTCCTTCGCTNNCGCC 5

RESULT 8  
LOCUS A86879 39 bp DNA linear PAT 22-JAN-2001  
DEFINITION Sequence 19 from Patent WO9838317.  
ACCESSION A86879  
VERSION A86879.1 GI:6735670  
KEYWORDS unclassified sequences.  
SOURCE unclassified sequences.  
ORGANISM unclassified sequences.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS Himmelsbach,M. and Eibl,J.  
TITLE FACTOR X ANALOGUES WITH A MODIFIED PROTEASE CLEAVAGE SITE  
JOURNAL Patent: WO 9838317-A 19 03-SEP-1998;  
FEATURES HIMMELSPACH MICHELE (AT); EIBL JOHANN (AT)  
source Location/Qualifiers  
1..39  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

ORIGIN

Query Match 23.8%; Score 18.8; DB 2; Length 39;  
Best Local Similarity 44.7%; Pred. No. 7.9e+04;  
Matches 17; Conservative 9; Mismatches 12; Indels 0; Gaps 0

QY 33 CCUUAUUGUACUUGCGGCUUAUUGUCUCUCCUUC 70  
DB 2 CCAGAATCGATTCTCGTGCTGCTGCTGCTGCTC 39

RESULT 9  
LOCUS BD070385 39 bp DNA linear PAT 27-AUG-2001  
DEFINITION Factor X-analogues with modified protease cleavage site.  
ACCESSION BD070385  
VERSION BD070385.1 GI:22615988  
KEYWORDS JP 2001513631-A/19.  
SOURCE unclassified sequences.  
ORGANISM unclassified sequences.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS Himmelsbach,M., Schlokot,U., Dornier,F., Andreas, Fisch and Eibl,J.  
TITLE Factor X-analogues with modified protease cleavage site  
JOURNAL Patent: JP 2001513631-A 19 04-SEP-2001;  
COMMENT BAXTER AG  
OS Unidentified  
PN JP 2001513631-A/19  
PD 04-SEP-2001  
PF 27-FEB-1998 JP 1998537062  
PR 27-FEB-1997 AT A 335/97  
PI MICHELE HIMMELSPACH,UWE SCHLOKOT,FRIEDRICH DORNIER,ANDREAS PI FISCH,JOHANN EIBL  
PC C12N15/57,C12N9/64,A61K38/48  
CC Strandedness: Single;  
CC Topology: Linear;  
CC Factor X-analogues





GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 13:52:37 ; Search time 314 Seconds  
(without alignments)  
1864.442 Million cell updates/sec

Title: US-10-604-726A-5135

Perfect score: 79

Sequence: 1 9gagggcggggagagacga.....ucucucuuucgcaccuuc 79

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 6021484

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq\_200701.\*

- 1: Geneseqn1980s.\*
- 2: Geneseqn1980s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*
- 14: Geneseqn2005s.\*
- 15: Geneseqn2006s.\*
- 16: Geneseqn2007s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	19.2	24.3	51	3 AAC10528	Aac10528 Human sec
C 2	19.2	24.3	80	12 ADM79864	Adm79864 DNA ligase
C 3	19.2	24.1	65	4 AAH68997	Aah68997 Human cer
C 4	18.8	23.8	39	2 AAV56769	Av56769 Human fac
C 5	18.8	23.8	72	6 AAD30987	Aad30987 Schizosac
C 6	18.8	23.8	72	6 AAD31044	Aad31044 Oligonuc
C 7	18.8	23.8	79	4 AAF70953	Aaf70953 bFGF DNA
C 8	18.8	23.8	80	2 AAT00367	Aat00367 Family 4
C 9	18.6	23.5	55	3 AAA09070	Aaa09070 Sense pri
C 10	18.6	23.5	65	6 ABN31245	Abn31245 Rat splc
C 11	18.6	23.5	70	15 AEG84737	Aeg84737 Hematolog
C 12	18.6	23.5	80	12 ADM95117	Adm95117 Rat antis
C 13	18.4	23.3	51	15 AEH27179	Aeh27179 Human acu
C 14	18.4	23.3	62	2 AAX59386	Aax59386 Saccharom
C 15	18.4	23.3	65	3 AAC11731	Aac11731 Human sec
C 16	18.4	23.3	80	12 ADP49484	Adp49484 Oligonuc
C 17	18.2	23.0	42	15 AEL27903	Ael27903 Primer fo

18	18.2	23.0	50	13	ADU25177	Adu25177 Retroelem
19	18.2	23.0	50	13	ADU22644	Adu22644 Human tra
C 20	18.2	23.0	60	6	ABN37704	Abn37704 Human spl
C 21	18.2	23.0	65	6	ABN28183	Abn28183 Rat prime
C 22	18	22.8	40	4	AAF55591	Aaf55591 PCR prime
C 23	18	22.8	40	5	AAF57180	Aaf57180 AAP-1 cDN
C 24	18	22.8	42	8	ABX79761	Abx79761 EST polym
C 25	18	22.8	50	4	AAL29974	Aal29974 Human SNP
C 26	18	22.8	51	4	AAL27582	Aal27582 Human SNP
C 27	18	22.8	51	4	AAL28619	Aal28619 Human SNP
C 28	18	22.8	54	13	ADR47436	Adr47436 Construct
C 29	18	22.8	80	12	ADM95450	Adm95450 Rat antis
C 30	17.8	22.5	44	15	AEJ30543	Aej30543 Strong co
C 31	17.8	22.5	44	15	AEJ90544	Aej90544 Respirato
C 32	17.8	22.5	57	15	AEJ95125	Aeg95125 Amyloid-b
C 33	17.8	22.5	60	14	ADY71737	Ady71737 Liver can
C 34	17.8	22.5	60	14	AEA35582	Aea35582 Analyte d
C 35	17.8	22.5	60	15	AEL55328	Ael55328 Murray re
C 36	17.8	22.5	60	15	AEL70698	Ael70698 Murray re
C 37	17.8	22.5	75	14	ACL60339	Act60339 Human col
C 38	17.6	22.3	50	6	ABZ00856	Abz00856 Human leu
C 39	17.6	22.3	59	2	AAV64733	Aav64733 HIV anti-
C 40	17.6	22.3	59	4	AAH24745	Aah24745 Nucleotid
C 41	17.6	22.3	59	8	ACA74051	Aca74051 Hepatitis
C 42	17.6	22.3	59	14	AED30192	Aed30192 Antiviral
C 43	17.6	22.3	60	6	ABN59362	Abn59362 Human spl
C 44	17.6	22.3	60	6	ABN59239	Abn59239 Human spl
C 45	17.4	22.0	36	6	ABK15487	Abk15487 Urokinase

#### ALIGNMENTS

#### RESULT 1

AAC10528/C  
ID AAC10528 standard; cDNA, 51 BP.

XX AC AAC10528;

DT 06-OCT-2000 (first entry)

DE Human secreted protein 5' EST, SEQ ID NO: 14603.

XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
XX KW gene therapy; chromosome mapping; ss.

XX OS Homo sapiens.

XX FN EPI033401-A2.

PD 06-SEP-2000.

PP 21-FEB-2000; 2000EP-00200610.

XX PR 26-FEB-1999; 99US-0122487P.

XX (GEST ) GENSET.

XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for  
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX Claim 1; SEQ ID NO 14603; 71pp + Sequence Listing; English.

CC The present sequence is one of a large number of 5' ESTs derived from  
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively  
CC identified within the present sequence. The 5' ESTs were prepared from  
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST  
CC sequences usually correspond mainly to the 3' untranslated region (UTR)





XX The invention relates to novel genes (AAH68727-AAH73383) associated with  
CC cervical cancer with cytostatic activity. The nucleic acids and encoded  
CC polypeptides are useful: to assess if a patient is afflicted with  
CC cervical cancer or has a pre-malignant condition; to monitor the  
CC progression of cervical cancer or a premalignant condition in a patient;  
CC and to select and/or assess the efficacy of a compound or therapy for  
CC inhibiting cervical cancer in a patient. The nucleic acids may also be  
CC useful for gene therapy  
XX

XX Sequence 65 BP; 19 A; 17 C; 19 G; 4 T; 0 U; 6 Other;  
SQ

Query Match 24.1%; Score 19; DB 4; Length 65;  
Best Local Similarity 37.5%; Pred. No. 9.1e+03;  
Matches 15; Conservative 10; Mismatches 15; Indels 0; Gaps 0;  
XX

Qy 40 UGUACUUGGGCUGUAUGUUGUCUCUUCUUGGCCACGUCC 79  
Db 44 TTTCTTCGTCNCGAANATCTTCTCTCGCTNNGGCC 5

RESULT 4  
AAV56769  
ID AAV56769 standard; DNA; 39 BP.  
XX  
XX AAV56769;  
AC  
XX  
DT 27-NOV-1998 (first entry)  
XX  
DE Human Factor X PCR primer #1017.  
XX  
XX Factor X; analogue; activation cleavage site; protease; bleeding; human;  
KW defect; Factor IX; Factor VII; Factor VIII; haemophilia; gene therapy;  
KW PCR primer; ss.  
XX  
XX Synthetic.  
OS Homo sapiens.  
XX  
XX W09838317-A1.  
PN  
XX  
XX 03-SEP-1998.  
PD  
XX  
XX 27-FEB-1998; 98WO-AT000045.  
PF  
XX  
XX 27-FEB-1997; 97AT-00000335.  
PR  
XX  
XX (IMMO ) IMMUNO AG.  
PA  
XX  
XX Himmlerspach M, Schlokot U, Dörner F, Fisch A, Eibl J;  
PI  
XX  
XX WPI; 1998-481211/41.  
DR  
XX  
XX New factor X analogues with processing site for protease not active on  
PT natural protein - and related DNA, is very stable and can be activated in  
PT vitro or in vivo without using animal protease(s), particularly for  
PT treating disorders of blood coagulation.  
XX  
XX  
PS Example 6; Page 41; 86pp; German.  
XX

AAV56751-V56775 are primers used in a method resulting in the production  
CC of novel human Factor X (F10) analogues. Such analogues have in the  
CC region of the natural F10a activation cleavage site, a modification that  
CC creates a processing site for a protease that does not naturally cleave  
CC F10 in this region. The proteins are used to generate, in vivo or in  
CC vitro, F10a analogues that can be used to control bleeding and for  
CC treating defects of factors IX, VII or VIII, e.g. in haemophiliacs who  
CC have developed antibodies to factors VIII and/or IX. The encoding nucleic  
CC acid can be used in gene therapy of the same conditions. The analogues  
CC have high stability and can be activated without use of animal enzymes  
CC such as trypsin. Only activation is affected, their activity is the same  
CC as the natural factor. The analogues can be isolated as a pure single-  
CC chain pro-protein (not usually possible because of rapid processing of  
CC the native precursor) and this converted to two-chain form by subsequent

[illegible]

Db	72	CCTTAATGTTCTTCATCATATAACCTTTTCTTCTGTTGGGAATC	27
XX	DE	bFGF DNA ligand #86.	
XX	XX	Ligand; basic fibroblast growth factor; bFGF; gene therapy; vascular;	
XX	KW	atherosclerosis; angioplasty; stability; ss.	
XX	OS	Unidentified.	
XX	PN	US6177557-B1.	
XX	XX	23-JAN-2001.	
XX	PD	05-AUG-1996; 96US-00687421.	
XX	PF	11-JUN-1990; 90US-00536428.	
XX	XX	10-JUN-1991; 91US-00714131.	
XX	PR	06-NOV-1992; 92US-00973333.	
XX	PR	10-FEB-1994; 94US-00195005.	
XX	PR	28-MAR-1994; 94US-00219012.	
XX	PA	(NEXS-) NEXSTAR PHARM INC.	
XX	XX	Janjic N, Gold L, Tasset D;	
XX	PI	WPI; 2001-158583/16.	
XX	XX	Novel nucleic acid ligands to basic fibroblast growth factor that are	
XX	DR	useful as inhibitors of basic fibroblast growth factors and 2'-amino	
XX	XX	modified RNA ligands, exhibit increased in vivo stability.	
XX	PT	Claim 1; Col 69-75; 153pp; English.	
XX	PT	The present invention relates to a purified and isolated non-naturally	
XX	CC	occurring DNA ligands to basic fibroblast growth factor (bFGF). The	
XX	CC	ligands are useful as part of gene therapy treatments and for diagnosing	
XX	CC	pathogenesis of vascular diseases including initiation and progression of	
XX	CC	atherosclerosis, acute coronary syndromes, vein graft disease and	
XX	CC	restenosis following coronary angioplasty. The ligands have improved	
XX	CC	stability in vivo	
XX	SQ	Sequence 79 BP; 18 A; 25 C; 13 G; 23 T; 0 U; 0 Other;	
XX	XX	Query Match 23.8%; Score 18.8; DB 4; Length 79;	
XX	XX	Best Local Similarity 38.7%; Pred. No. 1.1e+04;	
XX	XX	Matches 24; Conservative 11; Mismatches 27; Indels 0; Gaps	
XX	QY	17 ACGAGCGCUCUGCCGCCUUAUUGUCUGGCGUGUAUUGUCUCUUCUGCCACC	76
XX	Db	7 ACGATCTGACTAGCCACCCTGCTAGGAGTACCGACTCGATGTATGTACCTAGCTTAC	66
XX	QY	77 UC 78	
XX	Db	67 TC 68	
XX	XX	RESULT 8	
XX	XX	AAT00367	
XX	ID	AAT00367 standard; DNA; 80 BP.	
XX	XX	AAT00367;	
XX	XX	14-AUG-1996 (first entry)	
XX	DT	Family 4 bFGF DNA ligand b10 (experiment 2).	
XX	DE	Family 1; family 2; ligand; thrombin;	
XX	KW	systematic evolution of ligands by exponential enrichment; SELEX;	
XX	KW	heparin; selection; region of homology; inhibitor; ss.	
XX	XX	Synthetic.	
XX	XX	Key	Location/Qualifiers
XX	FT	misc feature 1..20	
XX	FT		

```
FT      /*tag= a
FT      /note= "Fixed region"
FT      21..58
FT      misc_feature
FT      /*tag= b
FT      /note= "Variable region"
FT      59..80
FT      misc_feature
FT      /*tag= c
FT      /note= "Fixed region"
FT      76
FT      misc_difference
FT      /*tag= d
FT      /note= "given in the specification as f"
XX      WO9521853-A1.
XX      17-AUG-1995.
XX      06-FEB-1995; 95WO-US001458.
XX      10-FEB-1994; 94US-00195005.
XX      28-MAR-1994; 94US-00219012.
XX      (NEXS-) NEXSTAR PHARM INC.
XX      Janjic N, Gold L, Tasset D;
XX      WPI; 1995-293073/38.
XX      Identification of ligands to basic fibroblast growth factor and thrombin
XX      - which can be modified for increased in vivo stability.
XX      Claim 21; Page 108; 236pp; English.
XX      The sequences given in AAT00282-394 represent DNA ligands to basic
XX      fibroblast growth factor (bFGF). These sequences were isolated using the
XX      primers and target regions given in AA098421-29 using systematic
XX      evolution of ligands by exponential enrichment (SELEX). DNA templates
XX      containing a region of 30 or 40 random nucleotides flanked by constant
XX      sequence regions, were synthesized. The constant regions were designed to
XX      be amplified by the primers. The primer 3p7.1PS has 2 biotin
XX      phosphoramidites and two additional A residues covalently attached to its
XX      5' terminus during synthesis. The random region was generated by
XX      utilising an equimolar mixture of the four nucleotides during oligo-
XX      nucleotide synthesis. Three pools of ssDNA were created that contain
XX      internal random regions. Each pool was incubated with bFGF at an excess
XX      of DNA to target. DNA bound to bFGF were selected by filtration. The
XX      selected single stranded DNA (ssDNA) was then amplified by PCR. A
XX      significant improvement in affinity of DNA ligands was seen after 10
XX      rounds of selection. Five distinct families of ssDNA were identified,
XX      based on regions of homology. Some sequences showed no obvious homology
XX      to the five families and are considered to be orphans
XX      Sequence 80 BP; 18 A; 25 C; 13 G; 23 T; 0 U; 1 Other;
XX      Query Match 23.8%; Score 18.8; DB 2; Length 80;
XX      Best Local Similarity 38.7%; Pred. No. 1.1e+04;
XX      Matches 24; Conservative 11; Mismatches 27; Indels 0; Gaps 0;
QY      17 ACAGCGGCGUCGCCCCUUAUUGUACUUGCGGCGUUAUGUCUUCUUCUCCGCCACC 76
DB      |||||
DB      7 ACAGTCCTGCTAGCCACCTGCATGAGGAGTACCCGACTCCGATTGTATGCTACCTAGCTTAC 66
QY      77 UC 78
DB      ||
DB      67 TC 68
RESULT 9
AAA09070/c
ID AAA09070 standard; DNA; 55 BP.
XX
AC AAA09070;
XX
DT 10-AUG-2000 (first entry)
XX
Sense primer for PROEX-1-beta-synuclein delta 1 construction.
XX
DE NACP/alpha-synuclein; beta-synuclein; beta-synuclein delta 1; mutant;
XX
KW primer; neurodegenerative; Alzheimers disease; Parkinsons disease;
XX
KW Lewy body disease; ss.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
FN WO200020020-A2.
XX
PD 13-APR-2000.
XX
XX 06-OCT-1999; 99WO-US023134.
XX
XX 06-OCT-1998; 98US-0103310P.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
XX Masliah E;
XX
XX WPI; 2000-303637/26.
XX
XX Screening treatments for neurodegenerative disease, such as Alzheimer's
XX
XX disease, comprises stimulating oxidative stress and measuring and
XX
XX aggregation of non-amyloid beta component /alpha-synuclein in neuronal
XX
XX cells.
XX
XX Disclosure; Page 45; 47pp; English.
XX
XX Human NACP/alpha-synuclein, human beta-synuclein and its mutants, beta-
XX
XX synuclein delta 1 and 2 were produced using the PROEX-1 6xHis expression
XX
XX system. PROEX-1-beta-synuclein delta 1 was constructed by a two step PCR
XX
XX protocol. This sense primer, corresponding to amino acids 73-83 of alpha-
XX
XX synuclein and amino acids 73-79 of beta-synuclein, was used with
XX
XX antisense primer BSYNNOT (AAA09071) encoding amino acids 129-134 of beta-
XX
XX synuclein and NotI site at its 5' end. The PCR product was combined to
XX
XX the product generated by primers AAA09068-69 by using BSYNNDE (AAA09068)
XX
XX and BSYNNOT. The invention concerns methods for screening treatments for,
XX
XX and treatment of, neurodegenerative disease. The methods comprise
XX
XX measuring aggregation of neurons of NACP/alpha-synuclein and stimulating
XX
XX expression of a non-amyloidogenic protein in order to reduce the level of
XX
XX aggregation. In the screening method, oxidative stress is stimulated in
XX
XX the neuronal cells by introduction of metal ions and hydrogen peroxide.
XX
XX The methods are useful for treating and screening treatments for
XX
XX neurodegenerative disease consisting of Alzheimer's disease, Parkinson's
XX
XX disease and Lewy body disease
XX
XX Sequence 55 BP; 16 A; 11 C; 23 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 23.5%; Score 18.6; DB 3; Length 55;
XX
XX Best Local Similarity 42.9%; Pred. No. 1.2e+04;
XX
XX Matches 21; Conservative 9; Mismatches 13; Indels 0; Gaps 0;
QY      18 CGAGCGGCGUCGCCCCUUAUUGUACUUGCGGCGUUAUGUCUUCUCC 66
DB      |||||
DB      49 CGATGTCCTGCCCCCTCCACTGCTCTCTGCGGCTACTGCTGTACACC 1
RESULT 10
ABN31245/c
ID ABN31245 standard; DNA; 65 BP.
XX
XX ABN31245;
XX
XX 15-JUL-2002 (first entry)
XX
XX Rat spliced transcript detection oligonucleotide SEQ ID NO:3993.
XX
XX Human; mouse; rat; splice transcript; detection; RNA transcript;
XX
XX splice variant; transcriptome; oligonucleotide library; ss.
XX
```





```
OS Synthetic.
OS Saccharomyces cerevisiae.
XX WO924580-A2.
XX 20-MAY-1999.
XX 09-NOV-1998; 98WO-US023874.
XX 07-NOV-1997; 97US-00965762.
XX (MILL-) MILLENNIUM PHARM INC.
XX Koltin Y, Gavrias V;
XX WPI; 1999-418430/35.
XX Aspergillus nidulans nucleic acids encoding essential proteins AN97,
PT AN80, AN85 and AN17.
XX Disclosure; Page 20; 78pp; English.
XX This is the one of a pair of primers (see also AAX59389) used in the PCR
CC amplification of a portion of the Saccharomyces cerevisiae genome
CC incorporating the newly identified D9798.4 essential gene (see AAX59382).
CC The primers hybridise to a portion of the 5' and 3' sequences flanking
CC the D9798.4 open reading frame and include nucleotides that are
CC homologous to the HIS3 selectable marker. The PCR product was used to
CC construct a yeast strain in which the D9798.4 gene was deleted in order
CC to confirm that this gene is essential for yeast survival. The D9798.4
CC gene is a homologue of the Aspergillus nidulans AN97 gene (see AAX59378).
CC The genes and their encoded polypeptides can be used to identify
CC homologous genes in other organisms and to identify novel antifungal or
CC anti-yeast agents
XX
XX Sequence 62 BP; 13 A; 19 C; 12 G; 18 T; 0 U; 0 Other;
SQ
Query Match 23.3%; Score 18.4; DB 2; Length 62;
Best Local Similarity 38.5%; Pred. No. 1.5e+04;
Matches 20; Conservative 11; Mismatches 21; Indels 0; Gaps 0;
QY 27 CUGGCCCUUAUUGUACUUGGGGCUUGUUGUCUUCUUCUUGCCACCUC 78
| | | | | : | : | : | : | : | : | : | : | : | : | : |
Db 8 CCGGCCCATCATGCAAGATCCTGATGTATTGACATTCTCTTGCCCTCCTC 59
| | | | | : | : | : | : | : | : | : | : | : | : | : |
RESULT 15
AAC11731
ID AAC11731 standard; cDNA; 65 BP.
XX
XX AAC11731;
XX
XX 06-OCT-2000 (first entry)
XX Human secreted protein 5' EST, SEQ ID NO: 15806.
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping; ss.
XX Homo sapiens.
XX
XX EP1033401-A2.
XX
XX 06-SEP-2000.
XX
XX 21-FEB-2000; 2000EP-00200610.
XX
XX 26-FEB-1999; 99US-0122487P.
XX
XX (GEST ) GENSET.
XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
XX
```

```
DR WPI; 2000-500381/45.
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX Claim 1; SEQ ID NO 15806; 71pp + Sequence Listing; English.
XX The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used
CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors
XX
XX Sequence 65 BP; 12 A; 15 C; 26 G; 12 T; 0 U; 0 Other;
SQ
Query Match 23.3%; Score 18.4; DB 3; Length 65;
Best Local Similarity 71.4%; Pred. No. 1.5e+04;
Matches 20; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 6 CGCGGGGAGACGACGAGCGGCUUGGCC 33
| | | | | : | : | : | : | : | : | : | : | : | : | : |
Db 17 CGCGGGGTGGAGACGCGCGGCTCTGTGCAC 44
| | | | | : | : | : | : | : | : | : | : | : | : | : |
Search completed: June 19, 2007, 14:04:59
Job time : 317 secs
```

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 14:28:35 ; Search time 129 Seconds  
(without alignments)  
1145.873 Million cell updates/sec

Title: US-10-604-726A-5135

Perfect score: 79

Sequence: 1 ggaaggcgaggagacga.....ucuccuucgaccucc 79

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 1528742

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_NA.\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1 COMB.seq.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5 COMB.seq.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A COMB.seq.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B COMB.seq.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7 COMB.seq.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H COMB.seq.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS COMB.seq.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP COMB.seq.\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE COMB.seq.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19.8	25.1	63	2	US-08-014-723-12
C 2	19.8	25.1	63	2	US-08-110-011A-12
C 3	19.2	24.3	51	3	US-09-513-999C-14603
C 4	19	24.1	65	2	US-08-014-723-11
C 5	19	24.1	65	2	US-08-110-011A-11
C 6	18.8	23.8	39	3	US-09-367-791A-19
C 7	18.8	23.8	54	3	US-08-444-818-753
C 8	18.8	23.8	79	3	US-08-687-421-415
C 9	18.4	23.3	62	3	US-08-965-762-27
C 10	18.4	23.3	62	3	US-09-911-927-27
C 11	18.4	23.3	62	3	US-09-911-882-27
C 12	18.4	23.3	62	3	US-09-911-888-27
C 13	18.4	23.3	65	3	US-09-513-999C-15806
C 14	18.2	23.0	65	2	US-08-086-410-28
C 15	18	22.8	42	3	US-09-475-947A-86
C 16	18	22.8	78	2	US-08-090-193-16
C 17	18	22.8	78	2	US-08-488-031-16
C 18	18	22.8	78	2	US-08-486-569-16
C 19	18	22.8	78	2	US-08-488-027-16
C 20	18	22.8	78	2	US-08-090-192-16
C 21	18	22.8	78	2	US-08-482-663-16
C 22	18	22.8	78	3	US-08-482-658-16
C 23	18	22.8	78	3	US-08-470-349-16

C 24	18	22.8	78	3	US-08-475-610-16	Sequence 16, Appl
C 25	18	22.8	78	7	PCT-US92-00277-16	Sequence 16, Appl
C 26	18	22.8	78	7	PCT-US92-00278-16	Sequence 16, Appl
C 27	17.8	22.5	77	5	US-09-844-508-25	Sequence 25, Appl
C 28	17.6	22.3	50	3	US-10-131-827-847	Sequence 847, App
C 29	17.6	22.3	50	5	US-10-131-831-847	Sequence 847, App
C 30	17.6	22.3	59	2	US-08-790-963-53	Sequence 53, Appl
C 31	17.6	22.3	59	3	US-09-371-774-53	Sequence 53, Appl
C 32	17.6	22.3	59	3	US-09-875-082-53	Sequence 53, Appl
C 33	17.4	22.0	72	2	US-08-433-126A-13	Sequence 13, Appl
C 34	17.4	22.0	72	2	US-08-433-124B-13	Sequence 13, Appl
C 35	17.4	22.0	72	3	US-08-376-413A-13	Sequence 13, Appl
C 36	17.4	22.0	72	7	PCT-US96-06059-13	Sequence 13, Appl
C 37	17.2	21.8	54	3	US-09-621-976-13448	Sequence 13448, A
C 38	17.2	21.8	60	4	US-09-804-980-240	Sequence 240, App
C 39	17.2	21.8	65	3	US-09-564-805-7	Sequence 7, Appli
C 40	17.2	21.8	65	3	US-09-434-382-7	Sequence 7, Appli
C 41	17.2	21.8	72	3	US-09-275-850-137	Sequence 137, App
C 42	17.2	21.8	72	3	US-09-907-111-137	Sequence 137, App
C 43	17.2	21.8	78	3	US-09-513-999C-15701	Sequence 15701, A
C 44	17	21.5	43	3	US-09-281-481A-12	Sequence 12, Appl
C 45	17	21.5	43	3	US-09-281-481A-14	Sequence 14, Appl

#### ALIGNMENTS

RESULT 1  
US-08-014-723-12/c  
; Sequence 12, Application US/08014723  
; Patent No. 5273962  
; GENERAL INFORMATION:  
; APPLICANT: Doi, Takeshi  
; APPLICANT: Iwasaki, Akio  
; APPLICANT: Saino, Yushi  
; APPLICANT: Kimura, Shigeru  
; APPLICANT: Okuchi, Masao  
; TITLE OF INVENTION: Thrombin-Binding Substance and Process  
; TITLE OF INVENTION: For Preparing the Same  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
; ADDRESSER: P.C.  
; STREET: 1755 Jefferson Davis Highway, Fourth Floor  
; CITY: Arlington  
; STATE: Virginia  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/014,723  
; FILING DATE: 19930208  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Oblon, No. 5273962man F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 80-071-0 CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)413-3000  
; TELEFAX: (703)413-2220  
; TELEX: 248855 OPAT UR  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 63 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-014-723-12

```

Query Match      25.18; Score 19.8; DB 2; Length 63;
Best Local Similarity 59.08; Pred No. 5.6e+02;
Matches 23; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

Qy      3 AGGCGGGGAGACAGCAGGGCCUCUGGCCCUUAUUG 41
||||| :|||:|||||:|||||:|||||:|||||:|||||:
Db      40 AGGTCTGACGACGAGGCCAGCGGGCTCTGGCACTACTCG 2

```

```

RESULT 2
US-08-110-011A-12/c
; Sequence 12, Application US/08110011A
; Patent No. 5354664
; GENERAL INFORMATION:
; APPLICANT: Doi, Takeshi
; APPLICANT: Iwasaki, Akio
; APPLICANT: Saino, Yushi
; Gaps 0;

```

APPLICANT: Kimura, Shigeru  
APPLICANT: Ohkuchi, Masao  
TITLE OF INVENTION: Thrombin-Binding Substance and Process  
TITLE OF INVENTION: For Preparing the Same

QY 1 GGAGGGCGGGGAGAGACGAGCGGCUCUGGGCCCTUUAUU 40  
DB 47 GGGCGCGGGCGGGCGGCCAGCAGCGGGCTCAGGGCCCTGCAGT 8

RESULT 4  
US-08-014-723-11  
Case: 08-014723  
Application US/08014723

SIR: 1.55 million base pairs  
;  
; CITY: Arlington  
; STATE: Virginia  
; ZIP: 22202  
;  
; GENERAL INFORMATION:  
; APPLICANT: Doi, Takeshi  
;  
; Sequence 11, approximately 88,000  
; Patent No. 5273962

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTED. IBM PC compatible

CONFIDENTIAL  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
APPLICANT: OHKUCHI, MASAO  
TITLE OF INVENTION: Thrombin-Binding Substance and Process for Preparing the Same  
INVENTOR: OHKUCHI, MASAO

;  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/110,011A  
 ; FILING DATE: 23-AUG-1993  
 ; TITLE OF INVENTION: FOR PREPARING THE SAME  
 ; NUMBER OF SEQUENCES: 18  
 ; CORRESPONDENCE ADDRESS: MAYER & NEUSTADT,  
 ;

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Oblon, No. 5354664man F.  
ADDRESSSEE: P.C.  
STREET: 1755 Jefferson Davis Highway, Fourth Floor  
ADDRESSSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & ROBBINS,

REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 80-073-0 DIV  
TELECOMMUNICATION INFORMATION:  
CITY: Arlington  
STATE: Virginia  
ZIP: 22202

TELEPHONE: (703)413-3000  
TELEPHONE: (703)413-2220  
TELEFAX: (703)413-2220  
TELEX SV. 240055 OMAT ITP  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
MEDIUM TYPE: DC compatible  
COMPARISON: IBM DC compatible

[illegible]

```

;
; LENGTH: 63 bases
;
; TYPE: nucleic acid
;
; STRANDEDNESS: single
;
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/014,723
;
; FILING DATE: 19930208
;

```

```

;
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid;
; DESCRIPTION: DNA (synthetic)
;
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblot, No. 5273962man F.
;

```

US-08-110-011A-12

Query Match	25.1%	Score 19.8;	DB 2;	Length 63;
REGISTRATION NUMBER: 24,618				
REFERENCE/DOCKET NUMBER: 80-071-0 CIP				
TELECOMMUNICATION INFORMATION:				

query matrix  
Best Local Similarity 59.0%; Pred. No. 5.6e+02;  
Matches 23; Conservative 4; Mismatches 12; Indels 0;  
Gaps 0;

LEBECOMBER, C. J.  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
C. J. LEBECOMBER, JR., LTD.

QY 3 AGGGCGGGGAGACGAGCGGCUCUGCCCCUUAUUG 41  
																							:
																							:
																							:

TELEX: 248855 OFAI UR  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:

QY

db 40 AGGTCGACGACGAGGCCAGCGGCGCTGGCGACGACGACG 2

```

RESULT 3
US-09-513-999C-14603/c
. Semence 14603. Application US/09513999C
;
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-014-723-11

```

US-06-011723 1A

Signed \_\_\_\_\_  
; Patent No. 6783961  
; GENERAL INFORMATION:  
GENERAL INFORMATION:  
INVENTOR: DUNCAN MILNE EDWARDS, J.B.  
ATTORNEY: \_\_\_\_\_  
Query Match 24.1%; Score 19; DB 2; Length 65;  
52.0%; Breed NO. 1.1e+03;  
\_\_\_\_\_

[illegible]



QY 3 AGGCGGGGAGACGAGCGGCGUCUGGCCCUUA 37  
 Db 30 AGTCGACGACGAGCGGCGCTCTGGCGACTGA 64

## RESULT 5

US-08-110-011A-11  
 ; Sequence 11, Application US/08110011A  
 ; Patent No. 5354664  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Doi, Takeshi  
 ; APPLICANT: Iwasaki, Akio  
 ; APPLICANT: Saino, Yushi  
 ; APPLICANT: Kimura, Shigeru  
 ; APPLICANT: Ohkuchi, Masao  
 ; TITLE OF INVENTION: Thrombin-Binding Substance and Process  
 ; TITLE OF INVENTION: For Preparing the Same  
 ; NUMBER OF SEQUENCES: 18  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
 ; ADDRESSEE: P.C.  
 ; STREET: 1755 Jefferson Davis Highway, Fourth Floor  
 ; CITY: Arlington  
 ; STATE: Virginia  
 ; ZIP: 22202  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/110,011A  
 ; FILING DATE: 23-AUG-1993  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: OBLON, NO. 5354664man.F.  
 ; REGISTRATION NUMBER: 24,618  
 ; REFERENCE/DOCKET NUMBER: 80-073-0 DIV  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (703)413-3000  
 ; TELEFAX: (703)413-2220  
 ; TELEX: 248855 OPAT UR  
 ; INFORMATION FOR SEQ ID NO: 11:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 65 bases  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: Other nucleic acid;  
 ; DESCRIPTION: DNA (synthetic)  
 ; US-08-110-011A-11

Query Match 24.1%; Score 19; DB 2; Length 65;  
 Best Local Similarity 62.9%; Pred. No. 1.1e+03;  
 Matches 22; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 3 AGGCGGGGAGACGAGCGGCGUCUGGCCCUUA 37  
 Db 30 AGTCGACGACGAGCGGCGCTCTGGCGACTGA 64

## RESULT 6

US-09-367-791A-19  
 ; Sequence 19, Application US/09367791A  
 ; Patent No. 6573071  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Himmelspach, Michele  
 ; Schlokot, Uwe  
 ; Dörner, Friedrich  
 ; Fisch, Andreas  
 ; Eibl, Johann  
 ; TITLE OF INVENTION: Factor X Analogues With

; a Modified Protease Cleavage Site  
 ; NUMBER OF SEQUENCES: 122  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, Eighth Floor  
 ; CITY: San Francisco  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94111-3834  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/367,791A  
 ; FILING DATE: 12-No. 6573071-1999  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: AT A 335/97  
 ; FILING DATE: 27-FEB-1997  
 ; APPLICATION NUMBER: WO PCT/AT98/00045  
 ; FILING DATE: 27-FEB-1998  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Ausenhus, Scott L.  
 ; REGISTRATION NUMBER: 42,471  
 ; REFERENCE/DOCKET NUMBER: 20695D-000700US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 576-0200  
 ; TELEFAX: (415) 576-0300  
 ; TELEX: <Unknown>  
 ; INFORMATION FOR SEQ ID NO: 19:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 39 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
 ; US-09-367-791A-19

Query Match 23.8%; Score 18.8; DB 3; Length 39;  
 Best Local Similarity 44.7%; Pred. No. 1.2e+03;  
 Matches 17; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 33 CCUUAUUGUACUUCGGCGGCUUAUUGUCUCUCCUUC 70  
 Db 2 CCAGATCGATTCTCGTGCTGTGTCGCCCTCTC 39

## RESULT 7

US-08-444-818-753/c  
 ; Sequence 753, Application US/08444818  
 ; Patent No. 6150087  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chien, David Y.  
 ; APPLICANT: Rutter, William J.  
 ; TITLE OF INVENTION: NANBV Diagnostics and Vaccines  
 ; NUMBER OF SEQUENCES: 777  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Chiron Corporation  
 ; STREET: 4560 Horton Street  
 ; CITY: Emeryville  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94608-2916  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/444,818

```

; FILING DATE: 10-JUNE-1991
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 753:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer JHC 13"
US-08-444-818-753

```

```

Query Match 23.8%; Score 18.8; DB 3; Length 54;
Best Local Similarity 48.1%; Pred. No. 1.3e+03;
Matches 26; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

```

```

QY 5 GCGGGGGGAGAGAGAGCGGCGCUCUAGGCGGCUUUAUUGUACUUGGCGGCUUUAU 58
Db 54 GCGGGGGGAGAGAGAGCGGCGCUCUAGGCGGCUUUAUUGUACUUGGCGGCUUUAU 1

```

# RESULT 8

```

US-08-687-421-415
; Sequence 415, Application US/08687421
; Patent No. 6177557
; GENERAL INFORMATION:
; APPLICANT: Gold, Larry
; APPLICANT: Janjic, Nebojsa
; APPLICANT: Tasset, Diane
; TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF BASIC
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR AND
; TITLE OF INVENTION: THROMBIN
; NUMBER OF SEQUENCES: 445
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,421
; FILING DATE: 08-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/195,005
; FILING DATE: 10-FEBRUARY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 22-APRIL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/219,012
; FILING DATE: 28-MARCH-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,333
; FILING DATE: 11-NOVEMBER-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131

```

```

; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX07/PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 415:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 79 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-687-421-415

```

```

Query Match 23.8%; Score 18.8; DB 3; Length 79;
Best Local Similarity 38.7%; Pred. No. 1.4e+03;
Matches 24; Conservative 11; Mismatches 27; Indels 0; Gaps 0;

```

```

QY 17 ACAGAGCGGCUUGGCGGCUUUAUUGUACUUGGCGGCUUUAUUGUACUUGGCGGCUU 76
Db 7 ACAGATCTGACTAGCCACCTGCATAGGAGTACCGACTCGGATTTGATGTCACCTAGCTTAC 66

```

```

QY 77 UC 78
Db 67 TC 68

```

# RESULT 9

```

US-08-965-762-27
; Sequence 27, Application US/08965762
; Patent No. 6280963
; GENERAL INFORMATION:
; APPLICANT: Koltin, Yigal
; APPLICANT: Gavrias, Victoria
; TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR USE
; FILE REFERENCE: 07334/062001
; CURRENT APPLICATION NUMBER: US/08/965,762
; CURRENT FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 62
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-08-965-762-27

```

```

Query Match 23.3%; Score 18.4; DB 3; Length 62;
Best Local Similarity 38.5%; Pred. No. 1.9e+03;
Matches 20; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

```

```

QY 27 CUGGCGGCUUUAUUGUACUUGGCGGCUUUAUUGUACUUGGCGGCUUUAUUGUACUUG 78
Db 8 CCGCGCCCATCATGCAAGATCCTGATGATTTGACATTTCTTTGGGCTCTC 59

```

# RESULT 10

```

US-09-911-927-27
; Sequence 27, Application US/09911927
; Patent No. 6461826
; GENERAL INFORMATION:
; APPLICANT: Koltin, Yigal
; APPLICANT: Gavrias, Victoria
; TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR USE
; FILE REFERENCE: 06286-062003
; CURRENT APPLICATION NUMBER: US/09/911,927
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 08/965,762
; PRIOR FILING DATE: 1997-11-07

```

	Query Match	23.3%	Score 18.4	DB 3	Length 62
	Best Local Similarity	38.5%	Pred. No. 1.9e+03		
	Matches	20	Conservative 11	Mismatches 21	Indels 0
	Gaps	0			
Qy	27	CUGGCCCCUUAUUGUACUUCUGGGCTUGUAUUGUCUCUCCUUUGCCACUUC	78		
Db	8	CCGCGGCCCATCGCAAGATCCTTGATGGTATTCACATTCCTCTGGCCTCTC	59		

RESULT 13  
US-09-513-999C-15806  
; Sequence 15806, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.

```

? TITLE OF INVENTION: Expressed sequence tags and encoded human proteins.
?
? Patent No. 6783961
?
? FILE REFERENCE: 59.US2.REG
?
? CURRENT APPLICATION NUMBER: US/09/513,999C
?
? CURRENT FILING DATE: 2000-02-24
?
? PRIOR APPLICATION NUMBER: US 60/122,487
?
? PRIOR FILING DATE: 1999-02-26
?
? NUMBER OF SEQ ID NOS: 36681
?
? SOFTWARE: Patent.pm
?
? SEQ ID NO 15806
?
? LENGTH: 65
?
? TYPE: DNA
?
? ORGANISM: Homo sapiens
?
? US-09-513-999C-15806

```

RESULT 14  
US-08-086-410-28  
; Sequence 28, Application US/08086410  
; Patent No. 5407822  
; GENERAL INFORMATION:  
; APPLICANT: LEPLATOIS, Pascal  
; APPLICANT: LOISON, Gerard

APPLICANT: SHIRE, DAVID  
 TITLE OF INVENTION: Artificial promoter for the expression  
 of proteins in yeast  
 NUMBER OF SEQUENCES: 37  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: FOLEY & LARDNER  
 STREET: King Street Station, Suite 500, 1800 Diagonal  
 STREET: Road, PO Box 299  
 CITY: ALEXANDRIA  
 STATE: VIRGINIA  
 COUNTRY: USA  
 ZIP: 22313-0299  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/086,410  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/768,083

Search completed: June 19, 2007, 15:45:42  
Job time : 131 secs

; CURRENT APPLICATION NUMBER: US/10/448,250

STATE: San Francisco  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/407,123  
FILING DATE: 04-Apr-2003  
CLASSIFICATION: <Unknown>  
PRIORITY INFORMATION DATA:  
APPLICATION NUMBER: US/09/367,791A  
FILING DATE: 12-NO. US20030181381A1-1999  
APPLICATION NUMBER: AT A 335/97  
FILING DATE: 27-FEB-1997  
APPLICATION NUMBER: WO PCT/AT98/00045  
FILING DATE: 27-FEB-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Ausenhuss, Scott L.  
REGISTRATION NUMBER: 42,471  
REFERENCE/DOCKET NUMBER: 20695D-000700US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
US-10-407-123-19  
Query Match 23.8%; Score 18.8; DB 7; Length 39;  
Best Local Similarity 44.7%; Pred. No. 7.6e+03;  
Matches 17; Conservative 9; Mismatches 12; Indels 0;  
QY 33 CCUUAUUGUACUUCGGGCTCGUAUUGUCUCCUUC 70  
DB 2 CCAGAAATGATTCCTCGTCTGGTGTGCTCCCTCTC 39  
RESULT 5  
US-09-918-740-15/c  
Sequence 15, Application US/09918740  
Publication No. US20030033626A1  
GENERAL INFORMATION:  
APPLICANT: Hahn, Frederick  
APPLICANT: Kuehnle, Adelheid  
TITLE OF INVENTION: Manipulation of genes of the mevalonate and  
FILE REFERENCE: KAS-103XC1  
CURRENT APPLICATION NUMBER: US/09/918,740  
CURRENT FILING DATE: 2001-07-31  
PRIOR APPLICATION NUMBER: 60/221,703  
PRIOR FILING DATE: 2000-07-31  
NUMBER OF SEQ ID NOS: 76  
SOFTWARE: Patent in version 3.0  
SEQ ID NO 15  
LENGTH: 72  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligonucleotide containing S. cerevisiae DNA  
US-09-918-740-15  
Query Match 23.8%; Score 18.8; DB 3; Length 72;  
Best Local Similarity 28.3%; Pred. No. 8.2e+03;







QY 41 GUACUUGGGGCUAGUAUUGUCUCUCCUUGGCCACCUC 79  
| | : : | : : : | : : : | : : : | : : : |  
Db .39 GTCGTCTCTCTCTMTATCGTTTCATCCTTTTCCCACCTAC 1

```
Query Match      23.0%; Score 18.2; DB 3; Length 60;
Best Local Similarity 45.2%; Pred. No. 1.3e+04;
Matches 14; Conservative. 9; Mismatches 8; Indels 0; Gaps 0;
```

Search completed: June 19, 2007, 15:35:39  
Job time : 745 secs

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 15:23:21 ; Search time 2967 Seconds  
(without alignments)  
274.926 Million cell updates/sec

Title: US-10-604-726A-5135

Perfect score: 79

Sequence: 1 99agggcg9gggagacga.....ucucuccuucgacaccucc 79

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 15754707 seqs, 5162687648 residues

Total number of hits satisfying chosen parameters: 22815532

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New.\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq1.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq2.\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq3.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq4.\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq5.\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq6.\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq1.\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq2.\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq3.\*
- 17: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq4.\*
- 18: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq5.\*
- 19: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq6.\*
- 20: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq7.\*
- 21: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq8.\*
- 22: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	32	40.5	32	11	US-10-536-560-26233
C 2	24.2	30.6	63	19	US-11-130-645A-109784
C 3	24.2	30.6	64	19	US-11-130-645A-22287
C 4	24.2	30.6	64	19	US-11-130-645A-169416
C 5	24.2	30.6	64	19	US-11-130-645A-348741
C 6	22.4	28.4	63	19	US-11-130-645A-498699
C 7	22.4	28.4	64	19	US-11-130-645A-245318
C 8	22.4	28.4	64	19	US-11-130-645A-51361
C 9	21.6	27.3	64	19	US-11-130-645A-156960
C 10	21.6	27.3	64	19	US-11-130-645A-243478
C 11	21.6	27.3	64	19	US-11-130-645A-385098

12	21.6	27.3	64	19	US-11-130-645A-426292	Sequence 426292,
13	21.6	27.3	64	19	US-11-130-645A-641194	Sequence 641194,
14	21.6	27.3	64	19	US-11-130-645A-660220	Sequence 660220,
15	21.6	27.3	65	19	US-11-130-645A-90177	Sequence 90177, A
C 16	20.6	26.1	63	19	US-11-130-645A-121147	Sequence 121147,
C 17	20.6	26.1	64	19	US-11-130-645A-524994	Sequence 524994,
C 18	20.6	26.1	64	19	US-11-130-645A-538349	Sequence 538349,
C 19	20	25.3	32	11	US-10-536-560-38260	Sequence 38260, A
C 20	20	25.3	64	19	US-11-130-645A-85134	Sequence 85134, A
C 21	20	25.3	64	19	US-11-130-645A-89154	Sequence 89154, A
C 22	20	25.3	64	19	US-11-130-645A-126839	Sequence 126839,
C 23	19.8	25.1	32	11	US-10-536-560-133728	Sequence 133728,
C 24	19.8	25.1	32	11	US-10-536-560-189867	Sequence 189867,
C 25	19.8	25.1	62	19	US-11-130-645A-39117	Sequence 39117, A
C 26	19.8	25.1	64	19	US-11-130-645A-145738	Sequence 145738,
C 27	19.8	25.1	64	19	US-11-130-645A-295048	Sequence 295048,
C 28	19.8	25.1	64	19	US-11-130-645A-393179	Sequence 393179,
C 29	19.8	25.1	64	19	US-11-130-645A-43301	Sequence 43301,
C 30	19.8	25.1	64	19	US-11-130-645A-546370	Sequence 546370,
C 31	19.8	25.1	64	19	US-11-130-645A-626880	Sequence 626880,
C 32	19.6	24.8	59	19	US-11-130-645A-108583	Sequence 108583,
C 33	19.6	24.8	64	19	US-11-130-645A-50209	Sequence 50209, A
C 34	19.6	24.8	64	19	US-11-130-645A-71244	Sequence 71244, A
C 35	19.6	24.8	64	19	US-11-130-645A-102927	Sequence 102927,
C 36	19.6	24.8	64	19	US-11-130-645A-276984	Sequence 276984,
C 37	19.6	24.8	64	19	US-11-130-645A-282851	Sequence 282851,
C 38	19.6	24.8	64	19	US-11-130-645A-386537	Sequence 386537,
C 39	19.6	24.8	64	19	US-11-130-645A-395089	Sequence 395089,
C 40	19.6	24.8	64	19	US-11-130-645A-395200	Sequence 395200,
C 41	19.6	24.8	64	19	US-11-130-645A-420624	Sequence 420624,
C 42	19.6	24.8	64	19	US-11-130-645A-481135	Sequence 481135,
C 43	19.6	24.8	64	19	US-11-130-645A-601445	Sequence 601445,
C 44	19.6	24.8	64	19	US-11-130-645A-646153	Sequence 646153,
C 45	19.6	24.8	64	19	US-11-130-645A-720580	Sequence 720580,

#### ALIGNMENTS

RESULT 1  
US-10-536-560-26233/c  
; Sequence 26233, Application US/10536560  
; Publication No. US20060257851A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; TITLE OF INVENTION: BIOS AND USES THEREOF  
; FILE REFERENCE: 06087.0300.PCUI3  
; CURRENT APPLICATION NUMBER: US/10/536.560  
; CURRENT FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 424571  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 26233  
; LENGTH: 32  
; TYPE: RNA  
; ORGANISM: Homo Sapiens  
US-10-536-560-26233

Query Match 40.5%; Score 32; DB 11; Length 32;  
Best Local Similarity 65.6%; Pred. No. 0.67;  
Matches 21; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY 25 CUCUGGCCCCUUAUUGUACUUGCGGCUUGA 56  
|:|||||:|||||:|||||:|||||:|||||:|  
Db 32 CTCUGGCCCCUUAUUGUACUUGCGGCTCGTA 1

#### RESULT 2

US-11-130-645A-109784/c  
; Sequence 109784, Application US/11130645A  
; Publication No. US20070050146A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwick, Itzhak

```

; APPLICANT: Amir, Avniel
; APPLICANT: Yael, Katov
; APPLICANT: Ranit, Alaronov
; TITLE OF INVENTION: MicroRNAs and Uses Thereof
; FILE REFERENCE: 06087.0202.CPUS13
; CURRENT APPLICATION NUMBER: US/11/130,645A
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: PCT/US05/16986
; PRIOR FILING DATE: 2005-05-14
; PRIOR APPLICATION NUMBER: US 10/709,577
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 10/709,572
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/666,340
; PRIOR FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: US 60/665,094
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/662,742
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US 60/593,329
; PRIOR FILING DATE: 2005-01-06
; PRIOR APPLICATION NUMBER: US 60/593,081
; PRIOR FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: US 60/522,860
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/522,457
; PRIOR FILING DATE: 2004-10-04
; Remaining Prior Application data removed - See
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 109784
; LENGTH: 63
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-130-645A-109784

```

	Query Match	30.6%;	Score 24.2;	DB 19;	Length 63;
	Best Local Similarity	37.8%;	Pred. No. 3.3e+02;		
	Matches 17; Conservative	15;	Mismatches 13;	Indels	0; Gaps 0;
QY	25	CUCUGGGCCCUUAAUUGUA	CUUCGGGCGUCGUUUGUCUCUCUUU	69	
db	56	CTCATGCCCAATCTTCTTC	TCTCGGGTCCTTTGTCCCTCCCTT	12	

RESULT 3  
US-11-130-645A-22287/c  
Sequence 22287, Application US/11130645A  
Publication No. US20070050146A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Itzhak  
APPLICANT: Amir, Avniel  
APPLICANT: Yael, Karov  
APPLICANT: Ranit, Aharonov  
TITLE OF INVENTION: Micrornas and Uses Thereof  
FILE REFERENCE: 06087.0202.CPUS13  
CURRENT APPLICATION NUMBER: US/11/130,645A  
CURRENT FILING DATE: 2005-05-16  
PRIOR APPLICATION NUMBER: PCT/US05/16986  
PRIOR FILING DATE: 2005-05-14  
PRIOR APPLICATION NUMBER: US 10/709,577  
PRIOR FILING DATE: 2004-05-14  
PRIOR APPLICATION NUMBER: US 10/709,572  
PRIOR FILING DATE: 2004-05-14  
PRIOR APPLICATION NUMBER: US 60/666,340  
PRIOR FILING DATE: 2005-03-30  
PRIOR APPLICATION NUMBER: US 60/665,094  
PRIOR FILING DATE: 2005-03-25  
PRIOR APPLICATION NUMBER: US 60/662,742  
PRIOR FILING DATE: 2005-03-17  
PRIOR APPLICATION NUMBER: US 60/593,329  
PRIOR FILING DATE: 2005-01-06  
PRIOR APPLICATION NUMBER: US 60/593,081

```

; PRIOR FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: US 60/522,860
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/522,457
; PRIOR FILING DATE: 2004-10-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22287
; LENGTH: 64
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-130-645A-22287

```

	Query Match	30.6%	Score 24.2	DB 19	Length 64
	Best Local Similarity	37.8%	Pred. No. 3.3e+02		
	Matches 17	Conservative 15	Mismatches 13	Indels 0	Gaps 0
QY	25	CUCUGGCCCCUUAUUGUAUCUUGGGCUCUGUAUUGUCUCUCCUUU	69		
Db	59	CTGCATCCCCCATCTCTCTACTTGGGTCCTTTTGGTCCCTCCCTT	15		

```

RESULT 4
US-11-130-645A-169416/c
; Sequence 169416, Application US/11130645A
; Publication No. US20070050146A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Amir, Avniel
; APPLICANT: Yael, Karov
; APPLICANT: Ranit, Aharonov
; TITLE OF INVENTION: Microarrays and Uses Thereof
; FILE REFERENCE: 06087.0202.CPUS13
; CURRENT APPLICATION NUMBER: US/11/130,645A
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: PCT/US05/16986
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 10/709,577
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 10/709,572
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/666,340
; PRIOR FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: US 60/665,094
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/662,742
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US 60/593,329
; PRIOR FILING DATE: 2005-01-06
; PRIOR APPLICATION NUMBER: US 60/593,081
; PRIOR FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: US 60/522,860
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/522,457
; PRIOR FILING DATE: 2004-10-04
; Remaining Prior Application data removed - See
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 169416
; LENGTH: 64
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-130-645A-169416

```

Query Match	30.6%	Score	24.2	DB 19	Length	64			
Best Local Similarity	37.8%	Pred. No.	3.3e+0%						
Matches	17	Conservative	15	Mismatches	13	Indels	0	Gaps	0

; PRIOR APPLICATION NUMBER: US 60/665,094  
 ; PRIOR FILING DATE: 2005-03-25  
 ; PRIOR APPLICATION NUMBER: US 60/662,742  
 ; PRIOR FILING DATE: 2005-03-17  
 ; PRIOR APPLICATION NUMBER: US 60/593,329  
 ; PRIOR FILING DATE: 2005-01-06  
 ; PRIOR APPLICATION NUMBER: US 60/593,081  
 ; PRIOR FILING DATE: 2004-12-08  
 ; PRIOR APPLICATION NUMBER: US 60/522,860  
 ; PRIOR FILING DATE: 2004-11-15  
 ; PRIOR APPLICATION NUMBER: US 60/522,457  
 ; PRIOR FILING DATE: 2004-10-04  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 760616  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 498699  
 ; LENGTH: 63  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-130-645A-498699

Query Match 28.4%; Score 22.4; DB 19; Length 63;  
 Best Local Similarity 48.2%; Pred. No. 1.3e+03;  
 Matches 27; Conservative 8; Mismatches 21; Indels 0; Gaps 0

QY 2 GAGGGCGGGGAGACGACGCGGCGUCUGCCGCCCUUAAUUGUACUUGCGGCGUCGUAU  
 DB 56 GTGGGGCGCTGGAGCGTGGCAGCACCTGTGGCCTCTGCATCACCCCTGGGGCAGGTCT

RESULT 7  
 US-11-130-645A-245318/c  
 ; Sequence 245318, Application US/11130645A  
 ; Publication No. US20070050146A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bentwich, Itzhak  
 ; APPLICANT: Amir, Avniel  
 ; APPLICANT: Yael, Karov  
 ; APPLICANT: Ranit, Aharonov  
 ; TITLE OF INVENTION: MicroRNAs and Uses Thereof  
 ; FILE REFERENCE: 06087.0202.CPUS13  
 ; CURRENT APPLICATION NUMBER: US/11/130,645A  
 ; CURRENT FILING DATE: 2005-05-16  
 ; PRIOR APPLICATION NUMBER: PCT/US05/16986  
 ; PRIOR FILING DATE: 2005-05-14  
 ; PRIOR APPLICATION NUMBER: US 10/709,577  
 ; PRIOR FILING DATE: 2004-05-14  
 ; PRIOR APPLICATION NUMBER: US 10/709,572  
 ; PRIOR FILING DATE: 2004-05-14  
 ; PRIOR APPLICATION NUMBER: US 60/666,340  
 ; PRIOR FILING DATE: 2005-03-30  
 ; PRIOR APPLICATION NUMBER: US 60/665,094  
 ; PRIOR FILING DATE: 2005-03-25  
 ; PRIOR APPLICATION NUMBER: US 60/662,742  
 ; PRIOR FILING DATE: 2005-03-17  
 ; PRIOR APPLICATION NUMBER: US 60/593,329  
 ; PRIOR FILING DATE: 2005-01-06  
 ; PRIOR APPLICATION NUMBER: US 60/593,081  
 ; PRIOR FILING DATE: 2004-12-08  
 ; PRIOR APPLICATION NUMBER: US 60/522,860  
 ; PRIOR FILING DATE: 2004-11-15  
 ; PRIOR APPLICATION NUMBER: US 60/522,457  
 ; PRIOR FILING DATE: 2004-10-04  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 760616  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 245318  
 ; LENGTH: 64  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-130-645A-245318

Query Match 28.4%; Score 22.4; DB 19; Length 64;



```

; Publication No. US20070050146A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Amir, Avniel
; APPLICANT: Yael, Karov
; APPLICANT: Ranit, Aharonov
; TITLE OF INVENTION: MicroRNAs and Uses Thereof
; FILE REFERENCE: 06087.0202.CPUS13
; CURRENT APPLICATION NUMBER: US/11/130,645A
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: PCT/US05/16986
; PRIOR FILING DATE: 2005-05-14
; PRIOR APPLICATION NUMBER: US 10/709,577
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 10/709,572
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/666,340
; PRIOR FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: US 60/665,094
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/662,742
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US 60/593,329
; PRIOR FILING DATE: 2005-01-06
; PRIOR APPLICATION NUMBER: US 60/593,081
; PRIOR FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: US 60/522,860
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/522,457
; PRIOR FILING DATE: 2004-10-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 426292
; LENGTH: 64
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-130-645A-426292

Query Match 27.3%; Score 21.6; DB 19; Length 64;
Best Local Similarity 58.2%; Pred.No. 2.5e+03;
Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 27 CUGGCCCCUUAUUGACUUCUGGGCGUGAUUGUCUCUCCUUC 70
    |||||
DB 14 CUGGCCCCUUCUGGGUUAUGAGCUGGAACUGUUCUACUUC 57
    |||||

RESULT 13
US-11-130-645A-641194
; Sequence 641194, Application US/11130645A
; Publication No. US20070050146A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Amir, Avniel
; APPLICANT: Yael, Karov
; APPLICANT: Ranit, Aharonov
; TITLE OF INVENTION: MicroRNAs and Uses Thereof
; FILE REFERENCE: 06087.0202.CPUS13
; CURRENT APPLICATION NUMBER: US/11/130,645A
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: PCT/US05/16986
; PRIOR FILING DATE: 2005-05-14
; PRIOR APPLICATION NUMBER: US 10/709,577
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 10/709,572
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/666,340
; PRIOR FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: US 60/665,094
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/662,742
; PRIOR FILING DATE: 2005-03-17

```

;; PRIOR APPLICATION NUMBER: US 60/593,329  
;; PRIOR FILING DATE: 2005-01-06  
;; PRIOR APPLICATION NUMBER: US 60/593,081  
;; PRIOR FILING DATE: 2004-12-08  
;; PRIOR APPLICATION NUMBER: US 60/522,860  
;; PRIOR FILING DATE: 2004-11-15  
;; PRIOR APPLICATION NUMBER: US 60/522,457  
;; PRIOR FILING DATE: 2004-10-04  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 760616  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 641194  
;; LENGTH: 64  
;; TYPE: RNA  
;; ORGANISM: Homo sapiens  
US-11-130-645A-641194

Query Match 27.3%; Score 21.6; DB 19; Length 64;  
Best Local Similarity 68.2%; Pred. No. 2.5e+03;  
Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 27 CUGGCCCCUUAUUGUACUUCGGGCGUUAUUGUACUUCUUCUUC 70  
Db 14 CUGGCCCCUUAUUGUACUUCGGGCGUUAUUGUACUUCUUCUUC 57

RESULT 14  
US-11-130-645A-660220  
;; Sequence 660220, Application US/11130645A  
;; Publication No. US20070050146A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Bentwich, Itzhak  
;; APPLICANT: Amir, Avniel  
;; APPLICANT: Yael, Karov  
;; TITLE OF INVENTION: MicroRNAs and Uses Thereof  
;; FILE REFERENCE: 06087.0202.CPUS13  
;; CURRENT APPLICATION NUMBER: US/11/130.645A  
;; CURRENT FILING DATE: 2005-05-16  
;; PRIOR APPLICATION NUMBER: PCT/US05/16986  
;; PRIOR FILING DATE: 2005-05-14  
;; PRIOR APPLICATION NUMBER: US 10/709,577  
;; PRIOR FILING DATE: 2004-05-14  
;; PRIOR APPLICATION NUMBER: US 10/709,572  
;; PRIOR FILING DATE: 2004-05-14  
;; PRIOR APPLICATION NUMBER: US 60/666,340  
;; PRIOR FILING DATE: 2005-03-30  
;; PRIOR APPLICATION NUMBER: US 60/665,094  
;; PRIOR FILING DATE: 2005-03-25  
;; PRIOR APPLICATION NUMBER: US 60/662,742  
;; PRIOR FILING DATE: 2005-03-17  
;; PRIOR APPLICATION NUMBER: US 60/593,329  
;; PRIOR FILING DATE: 2005-01-06  
;; PRIOR APPLICATION NUMBER: US 60/593,081  
;; PRIOR FILING DATE: 2004-12-08  
;; PRIOR APPLICATION NUMBER: US 60/522,860  
;; PRIOR FILING DATE: 2004-11-15  
;; PRIOR APPLICATION NUMBER: US 60/522,457  
;; PRIOR FILING DATE: 2004-10-04  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 760616  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 660220  
;; LENGTH: 64  
;; TYPE: RNA  
;; ORGANISM: Homo sapiens  
US-11-130-645A-660220

Query Match 27.3%; Score 21.6; DB 19; Length 64;  
Best Local Similarity 68.2%; Pred. No. 2.5e+03;  
Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 27 CUGGCCCCUUAUUGUACUUCGGGCGUUAUUGUACUUCUUCUUC 70

Db 14 CUGGCCCCUUAUUGUACUUCGGGCGUUAUUGUACUUCUUCUUC 57

RESULT 15  
US-11-130-645A-90177  
;; Sequence 90177, Application US/11130645A  
;; Publication No. US20070050146A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Bentwich, Itzhak  
;; APPLICANT: Amir, Avniel  
;; APPLICANT: Yael, Karov  
;; APPLICANT: Ranit, Aharonov  
;; TITLE OF INVENTION: MicroRNAs and Uses Thereof  
;; FILE REFERENCE: 06087.0202.CPUS13  
;; CURRENT APPLICATION NUMBER: US/11/130.645A  
;; CURRENT FILING DATE: 2005-05-16  
;; PRIOR APPLICATION NUMBER: PCT/US05/16986  
;; PRIOR FILING DATE: 2005-05-14  
;; PRIOR APPLICATION NUMBER: US 10/709,577  
;; PRIOR FILING DATE: 2004-05-14  
;; PRIOR APPLICATION NUMBER: US 10/709,572  
;; PRIOR FILING DATE: 2004-05-14  
;; PRIOR APPLICATION NUMBER: US 60/666,340  
;; PRIOR FILING DATE: 2005-03-30  
;; PRIOR APPLICATION NUMBER: US 60/665,094  
;; PRIOR FILING DATE: 2005-03-25  
;; PRIOR APPLICATION NUMBER: US 60/662,742  
;; PRIOR FILING DATE: 2005-03-17  
;; PRIOR APPLICATION NUMBER: US 60/593,329  
;; PRIOR FILING DATE: 2005-01-06  
;; PRIOR APPLICATION NUMBER: US 60/593,081  
;; PRIOR FILING DATE: 2004-12-08  
;; PRIOR APPLICATION NUMBER: US 60/522,860  
;; PRIOR FILING DATE: 2004-11-15  
;; PRIOR APPLICATION NUMBER: US 60/522,457  
;; PRIOR FILING DATE: 2004-10-04  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 760616  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 90177  
;; LENGTH: 65  
;; TYPE: RNA  
;; ORGANISM: Homo sapiens  
US-11-130-645A-90177

Query Match 27.3%; Score 21.6; DB 19; Length 65;  
Best Local Similarity 68.2%; Pred. No. 2.5e+03;  
Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 27 CUGGCCCCUUAUUGUACUUCGGGCGUUAUUGUACUUCUUCUUC 70  
Db 15 CUGGCCCCUUAUUGUACUUCGGGCGUUAUUGUACUUCUUCUUC 58

Search completed: June 19, 2007, 16:25:10  
Job time : 2967 secs

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 14:05:10 ; Search time 2495 Seconds  
(without alignments)  
1964.425 Million cell updates/sec

Title: US-10-604-726A-5135

Perfect score: 79

Sequence: 1 ggagggcggggagagacga.....ucucuuuugccaccucc 79

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 624300

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.\*

1: gb\_est1.\*

2: gb\_est3.\*

3: gb\_est4.\*

4: gb\_est5.\*

5: gb\_est6.\*

6: gb\_est7.\*

7: gb\_est8.\*

8: gb\_est9.\*

9: gb\_est10.\*

10: gb\_est11.\*

11: gb\_est12.\*

12: gb\_est13.\*

13: gb\_est14.\*

14: gb\_est15.\*

15: gb\_est16.\*

16: gb\_est17.\*

17: gb\_est18.\*

18: gb\_est19.\*

19: gb\_est20.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21.6	27.3	76	5	BX728792
2	20.6	26.1	76	12	EC019237
3	19.8	25.1	78	19	CT351516
4	19.6	24.8	71	17	CW020424
5	19.4	24.6	58	19	CR076775
6	19.4	24.6	71	13	DN441479
7	19.4	24.6	76	16	BZ381406
8	19.4	24.6	76	17	CW236987
9	19.4	24.6	78	11	H25883
10	19.4	24.6	78	12	EC034520
11	19.2	24.3	46	1	A1360975
12	19.2	24.3	50	7	AU105862
13	19.2	24.3	66	17	CW022621
14	19.2	24.3	78	18	DX045680

C	15	19.2	24.3	79	1	AI539851
	16	19	24.1	51	19	BX289701
	17	19	24.1	65	11	EC687830
C	18	19	24.1	78	10	CR587313
C	19	19	24.1	79	15	AZ605020
	20	18.8	23.8	46	1	AA569383
C	21	18.8	23.8	61	8	CB046583
	22	18.8	23.8	67	12	DY248960
C	23	18.8	23.8	78	3	CD945332
	24	18.8	23.8	78	3	BJ029975
	25	18.6	23.5	37	15	AZ769939
	26	18.6	23.5	48	15	AZ767626
C	27	18.6	23.5	73	1	AA912015
	28	18.6	23.5	73	12	EB988681
	29	18.6	23.5	79	12	EB783239
	30	18.4	23.3	50	7	AU103010
	31	18.4	23.3	50	7	AU103012
	32	18.4	23.3	69	12	EC054167
C	33	18.4	23.3	70	11	EC693412
	34	18.4	23.3	74	16	CC458134
	35	18.4	23.3	77	13	DR337378
C	36	18.2	23.0	32	17	CL300541
	37	18.2	23.0	50	7	AU102976
	38	18.2	23.0	52	15	AZ769999
	39	18.2	23.0	58	1	AI554529
C	40	18.2	23.0	63	8	CF297944
	41	18.2	23.0	73	19	ATH551807
	42	18.2	23.0	77	19	CR106056
C	43	18.2	23.0	79	12	EC459732
	44	18	22.8	64	15	AZ921047
C	45	18	22.8	65	19	DE108298

#### ALIGNMENTS

RESULT 1  
LOCUS BX728792 76 bp mRNA linear EST 18-NOV-2003  
DEFINITION BX728792 XGC-tadpole Xenopus tropicalis cDNA clone TTPA036j08 5', mRNA sequence.  
ACCESSION BX728792  
VERSION BX728792.1 GI:38401533  
KEYWORDS EST.  
SOURCE Xenopus tropicalis (western clawed frog)  
ORGANISM Xenopus tropicalis  
REFERENCE 1 (bases 1 to 76)  
AUTHORS Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.  
TITLE Sanger Xenopus tropicalis EST project 2001 (11\_2003)  
JOURNAL Unpublished (2003)  
COMMENT Contact: Croning MDR  
Sanger Institute  
Hinnton, Cambridgeshire, CB10 1SA, UK  
Email: trop@sanger.ac.uk  
Sanger Xenopus tropicalis EST project 2001  
TROPICALIS\_SEQUENCE ID: TTPA036j08.pikSP6  
Sequencing primer: SP6  
This sequence is from a Xenopus Gene Collection (XGC) library  
constructed by Nigel Garrett.  
cDNA was oligo dT primed from sug of poly A+ RNA from tadpole  
embryos. EcoRI-NotI cut cDNA was then ligated into pCS107 with  
EcoRI at the 5' end and NotI at the 3' end.  
Vector: pCS107; Site 1: EcoRI; Site 2: NotI  
Host: Escherichia coli DH10B.  
Host location/Qualifiers  
1..76  
/organism="Xenopus tropicalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8364"  
/clone="TTPA036j08"





```

/cell_line="E14"
/clone_lib="TIGEM gene trap library"
/note="vector: pFLIP1"

ORIGIN
Query Match      24.8%; Score 19.6; DB 17; Length 71;
Best Local Similarity 52.0%; Pred. No. 8.7e+04;
Matches 26; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

Qy 1 GGGGGGGGGGAGAGACGAGCGGCGUCUCUGGCCCUAAUUGUACUUCGGG 50
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 GGGGGGGGGGGAACGAGCGGGGGCCCCCCTTTTATACAGGGG 50

RESULT 5
LOCUS CR076775 58 bp DNA linear GSS 05-JUL-2004
DEFINITION Reverse strand read from insert in 3'HPRT insertion targeting and
            chromosome engineering clone MHP113c17, genomic survey sequence.
ACCESSION CR076775
VERSION GSS; genome survey sequence; MICR.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 58)
AUTHORS Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
Rogers,J. and Bradley,A.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICR
FEATURES             Location/Qualifiers
     source           1..58
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /clone="MHP113c17"
                     /clone_lib="MHP"

ORIGIN
Query Match      24.6%; Score 19.4; DB 19; Length 58;
Best Local Similarity 75.9%; Pred. No. 1e+05;
Matches 22; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GAGGGCGGGGAGAGACGAGCGGCGUCUGG 30
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 21 GAGGGCGGGGAGAGCGGGGGCGAGCACTGG 49

RESULT 6
LOCUS DN441479 71 bp mRNA linear EST 08-MAR-2005
DEFINITION LIB5338-102-A1-K2-G6 LIB5338 Canis familiaris cDNA clone
            CLN14241789, mRNA sequence.
ACCESSION DN441479
VERSION DN441479.1 GI:60637724
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Caniformia; Canidae;
Canis.
REFERENCE 1 (bases 1 to 71)
AUTHORS Staten,N.R.
TITLE Direct Submission (Staten,N.R.)
JOURNAL Unpublished (2005)
COMMENT Contact: Nick Staten
        Tel: 636 247 6855
        Email: nicholas.r.staten@pfizer.com.
        Location/Qualifiers

ORIGIN
Query Match      24.6%; Score 19.4; DB 16; Length 76;
Best Local Similarity 37.7%; Pred. No. 1e+05;
Matches 20; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

Qy 14 GAGAGCGGCGGCGUCUGGCCCUAAUUGUACUUCGGGCGUAGUCUCUCC 66

```

```

1..71
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/clone="CLN14241789"
/tissue_type="kidney"
/lab_host="DH10B"
/clone_lib="LIB5338"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; whole
organ"

ORIGIN
Query Match      24.6%; Score 19.4; DB 13; Length 71;
Best Local Similarity 45.3%; Pred. No. 1e+05;
Matches 24; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

Qy 5 GGGGGGGGAGAGACGAGCGGCGUCUGGCCCUAAUUGUACUUCGGGCGUAGU 57
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 17 GGGGGGAGCGGGAGACCGCGGCCCGCCACCAATTGTTCTCTTCGTCTTCT 69

RESULT 7
LOCUS BZ381406 76 bp DNA linear GSS 26-NOV-2002
DEFINITION BZ381406 SALK_116666.43.10.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_116666.43.10.x, genomic
            survey sequence.
ACCESSION BZ381406
VERSION BZ381406.1 GI:25475317
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 76)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
        Salk Institute Genomic Analysis Laboratory (SIGNAL)
        The Salk Institute for Biological Studies
        10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
        Tel: 858 453 4100 x1752
        Fax: 858 558 6379
        Email: ecker@salk.edu
        This is single pass sequence recovered from the left border of
        TDNA. This sequence lies within an annotated exon of At5g61190.
        Class: TDNA tagged.
        Location/Qualifiers
     source           1..76
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /ecotype="Col-0"
                     /db_xref="taxon:3702"
                     /clone="SALK_116666.43.10.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains one or more TDNA insertion
                     elements. The resultant fragment for each line was
                     directly sequenced to determine the genomic sequence at
                     the site of insertion. Details of the protocols used can
                     be found at http://signal.salk.edu/tdna\_protocols.html"

ORIGIN
Query Match      24.6%; Score 19.4; DB 16; Length 76;
Best Local Similarity 37.7%; Pred. No. 1e+05;
Matches 20; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

Qy 14 GAGAGCGGCGGCGUCUGGCCCUAAUUGUACUUCGGGCGUAGUCUCUCC 66

```







POLYA=No. Location/Qualifiers  
 1. .79  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2204193"  
 /tissue\_type="poorly-differentiated endometrial  
 adenocarcinoma, 2 pooled tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Ut3"  
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.45 Kb. Life Technologies catalog #: 11541-018"

ORIGIN

Query Match 24.1%; Score 19.2; DB 1; Length 79;  
 Best Local Similarity 39.1%; Pred. No. 1.2e+05;  
 Matches 25; Conservative 11; Mismatches 28; Indels 0; Gaps 0;

QY 7 CCGGGGAGAGACGAGCGGCGUCGCGCCUUAUUGUACUUCGGCGUCGUUUGUCUCC 66  
 ||||| ||||| ||| : ||| : : : ||||| : : |||  
 Db 65 CCGGGGCGGCGCGTCCGCTTTCCCTTTTTCCTCCCGGGGGTTTGGGGCCCC 6

QY 67 UUUC 70  
 : :  
 Db 5 TTCC 2

Search completed: June 19, 2007, 15:23:11  
 Job time : 2499 secs

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 12:41:00 ; Search time 1106 Seconds  
(without alignments)  
1499.898 Million cell updates/sec

Title: US-10-604-726A-5136  
Perfect score: 24  
Sequence: 1 uauugucucuccuugccaccuc 24

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 2038054

Minimum DB seq length: 0  
Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*  
1: gb\_env.\*  
2: gb\_pat.\*  
3: gb\_ph.\*  
4: gb\_pl.\*  
5: gb\_pr.\*  
6: gb\_ro.\*  
7: gb\_sts.\*  
8: gb\_sy.\*  
9: gb\_un.\*  
10: gb\_vi.\*  
11: gb\_ov.\*  
12: gb\_hcg.\*  
13: gb\_in.\*  
14: gb\_om.\*  
15: gb\_ba.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15.6	65.0	24	2	AR010008 Sequence
C 2	15.6	65.0	24	2	AR010025 Sequence
C 3	15.6	65.0	24	2	AR034743 Sequence
C 4	15.6	65.0	24	2	AR034760 Sequence
C 5	15.6	65.0	24	2	I24740 Sequence 3
C 6	15.6	65.0	24	2	I24752 Sequence 15
C 7	15.2	63.3	21	2	AR877903 Sequence
C 8	15.2	63.3	22	2	AR877901 Sequence
C 9	14.4	60.0	18	2	AR072296 Sequence
C 10	14.4	60.0	18	2	I26407 Sequence 99
C 11	14.4	60.0	20	2	AR877905 Sequence
C 12	14.2	59.2	21	2	I28585 Sequence 38
C 13	14.2	59.2	21	2	I58747 Sequence 38
C 14	14.2	59.2	25	2	AX649750 Sequence
C 15	14.2	59.2	25	2	AX649751 Sequence
C 16	14.2	59.2	25	2	AX649752 Sequence
C 17	14.2	59.2	25	2	AX649753 Sequence
C 18	14.2	59.2	25	2	AX649754 Sequence

C 19	14.2	59.2	25	2	AX649755 Sequence
C 20	14.2	59.2	25	2	AX649756 Sequence
C 21	14	58.3	24	2	A24320 LST3 Primer
C 22	14	58.3	24	2	AR010021 Sequence
C 23	14	58.3	24	2	AR034756 Sequence
C 24	14	58.3	24	2	I24749 Sequence 12
C 25	13.8	57.5	17	2	AX648244 Sequence
C 26	13.8	57.5	20	2	BD268715 Inhibitor
C 27	13.8	57.5	20	2	CQ764854 Sequence
C 28	13.8	57.5	20	2	AR229112 Sequence
C 29	13.8	57.5	20	2	AR281375 Sequence
C 30	13.8	57.5	20	2	AR304584 Sequence
C 31	13.8	57.5	20	2	AR312823 Sequence
C 32	13.8	57.5	20	2	AR337580 Sequence
C 33	13.8	57.5	20	2	AR590429 Sequence
C 34	13.8	57.5	25	2	AX649748 Sequence
C 35	13.8	57.5	25	2	AX649749 Sequence
C 36	13.6	56.7	20	2	BD411373 Method fo
C 37	13.6	56.7	22	2	CS113604 Sequence
C 38	13.4	55.8	17	2	AR072297 Sequence
C 39	13.4	55.8	17	2	DD023799 YEAST-BAS
C 40	13.4	55.8	17	2	I26408 Sequence 10
C 41	13.4	55.8	17	2	AX469671 Sequence
C 42	13.4	55.8	18	2	BD345059 Antisense
C 43	13.4	55.8	18	2	CS177232 Sequence
C 44	13.4	55.8	18	2	AR882372 Sequence
C 45	13.4	55.8	18	2	AX191825 Sequence

# ALIGNMENTS

RESULT 1	AR010008/c	AR010008	Sequence 20 from patent US 5756684.	24 bp	DNA	linear	PAT 04-DEC-1998
LOCUS	AR010008/c	AR010008	Sequence 20 from patent US 5756684.	24 bp	DNA	linear	PAT 04-DEC-1998
DEFINITION	AR010008	AR010008	Sequence 20 from patent US 5756684.	24 bp	DNA	linear	PAT 04-DEC-1998
ACCESSION	AR010008	AR010008	Sequence 20 from patent US 5756684.	24 bp	DNA	linear	PAT 04-DEC-1998
VERSION	AR010008.1	GI:3968813	Sequence 20 from patent US 5756684.	24 bp	DNA	linear	PAT 04-DEC-1998
KEYWORDS	Unknown.	Unknown.	Sequence 20 from patent US 5756684.	24 bp	DNA	linear	PAT 04-DEC-1998
SOURCE	Unknown.	Unknown.	Sequence 20 from patent US 5756684.	24 bp	DNA	linear	PAT 04-DEC-1998
ORGANISM	Unknown.	Unknown.	Sequence 20 from patent US 5756684.	24 bp	DNA	linear	PAT 04-DEC-1998
REFERENCE	1 (bases 1 to 24)	Unknown.	Sequence 20 from patent US 5756684.	24 bp	DNA	linear	PAT 04-DEC-1998
AUTHORS	Johnson, E.M. and Bergemann, A.D.	Unknown.	Sequence 20 from patent US 5756684.	24 bp	DNA	linear	PAT 04-DEC-1998
TITLE	Cloning and expression of PUR protein	Unknown.	Sequence 20 from patent US 5756684.	24 bp	DNA	linear	PAT 04-DEC-1998
JOURNAL	Patent: US 5756684-A 20 26-MAY-1998;	Unknown.	Sequence 20 from patent US 5756684.	24 bp	DNA	linear	PAT 04-DEC-1998
FEATURES	Location/Qualifiers	Unknown.	Sequence 20 from patent US 5756684.	24 bp	DNA	linear	PAT 04-DEC-1998
source	1..24	Unknown.	Sequence 20 from patent US 5756684.	24 bp	DNA	linear	PAT 04-DEC-1998
ORIGIN	/organism="unknown"	Unknown.	Sequence 20 from patent US 5756684.	24 bp	DNA	linear	PAT 04-DEC-1998
	/mol_type="unassigned DNA"	Unknown.	Sequence 20 from patent US 5756684.	24 bp	DNA	linear	PAT 04-DEC-1998

Query Match 65.0%; Score 15.6; DB 2; Length 24;  
Best Local Similarity 50.0%; Pred. No. 2e+04;  
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 3 UUGUCUCUCUUGCCACCUC 24  
Dy 23 TTTCCTCTCCCTCCACCCTC 2

RESULT 2	AR010025	AR010025	Sequence 38 from patent US 5756684.	24 bp	DNA	linear	PAT 04-DEC-1998
LOCUS	AR010025	AR010025	Sequence 38 from patent US 5756684.	24 bp	DNA	linear	PAT 04-DEC-1998
DEFINITION	AR010025	AR010025	Sequence 38 from patent US 5756684.	24 bp	DNA	linear	PAT 04-DEC-1998
ACCESSION	AR010025	AR010025	Sequence 38 from patent US 5756684.	24 bp	DNA	linear	PAT 04-DEC-1998
VERSION	AR010025.1	GI:3968830	Sequence 38 from patent US 5756684.	24 bp	DNA	linear	PAT 04-DEC-1998
KEYWORDS	Unknown.	Unknown.	Sequence 38 from patent US 5756684.	24 bp	DNA	linear	PAT 04-DEC-1998
SOURCE	Unknown.	Unknown.	Sequence 38 from patent US 5756684.	24 bp	DNA	linear	PAT 04-DEC-1998
ORGANISM	Unknown.	Unknown.	Sequence 38 from patent US 5756684.	24 bp	DNA	linear	PAT 04-DEC-1998
REFERENCE	1 (bases 1 to 24)	Unknown.	Sequence 38 from patent US 5756684.	24 bp	DNA	linear	PAT 04-DEC-1998
AUTHORS	Johnson, E.M. and Bergemann, A.D.	Unknown.	Sequence 38 from patent US 5756684.	24 bp	DNA	linear	PAT 04-DEC-1998

```

TITLE      Cloning and expression of pur protein
JOURNAL    Patent: US 5756684-A 38 26-MAY-1998;
FEATURES   Location/Qualifiers
           source
           1..24
           /organism="unknown"
           /mol_type="unassigned DNA"

ORIGIN
Query Match      65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 2e+04;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY      3 UUGUCUCUCCUUUGCCACCUC 24
       ::|||::|::|::|::|::|::|
Db      2 TTTTCTCTCCCTCCACCACCTC 23

RESULT 3
AR034743/c      24 bp      DNA
LOCUS          Sequence 20 from patent US 5869622.
DEFINITION
ACCESSION      AR034743
VERSION        AR034743.1 GI:5950348
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 24)
AUTHORS       Johnson,E.M. and Bergemann,A.D.
TITLE         Monoclonal antibodies to the pur protein
JOURNAL       Patent: US 5869622-A 20 09-FEB-1999;
FEATURES      Location/Qualifiers
           source
           1..24
           /organism="unknown"
           /mol_type="unassigned DNA"

ORIGIN
Query Match      65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 2e+04;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY      3 UUGUCUCUCCUUUGCCACCUC 24
       ::|||::|::|::|::|::|::|
Db      2 TTTTCTCTCCCTCCACCACCTC 23

RESULT 4
AR034760      24 bp      DNA
LOCUS          Sequence 38 from patent US 5869622.
DEFINITION
ACCESSION      AR034760
VERSION        AR034760.1 GI:5950365
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 24)
AUTHORS       Johnson,E.M. and Bergemann,A.D.
TITLE         Monoclonal antibodies to the pur protein
JOURNAL       Patent: US 5869622-A 38 09-FEB-1999;
FEATURES      Location/Qualifiers
           source
           1..24
           /organism="unknown"
           /mol_type="unassigned DNA"

ORIGIN
Query Match      65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 2e+04;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY      3 UUGUCUCUCCUUUGCCACCUC 24
       ::|||::|::|::|::|::|::|
Db      2 TTTTCTCTCCCTCCACCACCTC 23

RESULT 5
I24740/c      24 bp      DNA
LOCUS          Sequence 3 from patent US 5545551.
DEFINITION
ACCESSION      I24740
VERSION        I24740.1 GI:1604610
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 24)
AUTHORS       Johnson,E.M. and Bergmann,A.D.
TITLE         Cloning and expression of pur protein
JOURNAL       Patent: US 5545551-A 3 13-AUG-1996;
FEATURES      Location/Qualifiers
           source
           1..24
           /organism="unknown"
           /mol_type="unassigned DNA"

ORIGIN
Query Match      65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 2e+04;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY      3 UUGUCUCUCCUUUGCCACCUC 24
       ::|||::|::|::|::|::|::|
Db      23 TTTTCTCTCCCTCCACCACCTC 23

RESULT 6
I24752      24 bp      DNA
LOCUS          Sequence 15 from patent US 5545551.
DEFINITION
ACCESSION      I24752
VERSION        I24752.1 GI:1604622
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 24)
AUTHORS       Johnson,E.M. and Bergmann,A.D.
TITLE         Cloning and expression of pur protein
JOURNAL       Patent: US 5545551-A 15 13-AUG-1996;
FEATURES      Location/Qualifiers
           source
           1..24
           /organism="unknown"
           /mol_type="unassigned DNA"

ORIGIN
Query Match      65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 2e+04;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY      3 UUGUCUCUCCUUUGCCACCUC 24
       ::|||::|::|::|::|::|::|
Db      23 TTTTCTCTCCCTCCACCACCTC 23

RESULT 7
AR877903/c      21 bp      DNA
LOCUS          Sequence 2144 from patent US 7045289.
DEFINITION
ACCESSION      AR877903
VERSION        AR877903.1 GI:111975391
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 21)
AUTHORS       Allawi,H., Bartholomay,C.T., Chehak,L., Curtis,M.L., Eis,P.S.,
              Hall,J.G., Ip,H.S., Kaiser,M., Kwiatkowski,R.W. Jr., Lukowiak,A.A.,
```



**TITLE** Primers and methods for detecting mutations in the procollagen II gene (COL2A1) that indicate a genetic predisposition for a COL2A1-associated disease

```
Best Local Similarity 56.2%; Pred. No. 7.1e+04;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 5 GUCUCUCUUCGCCA 20
Db 19 GTCTCTCTTTGCCA 4

RESULT 12
LOCUS 128585/21 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 38 from patent US 5571937.
ACCESSION 128585
VERSION 128585.1 GI:1819361
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Watanabe,K.A., Ren,W.-Y. and Weil,R.
TITLE Complementary DNA and toxins
JOURNAL Patent: US 5571937-A 38 05-NOV-1996;
FEATURES
source
1..21
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 59.2%; Score 14.2; DB 2; Length 21;
Best Local Similarity 36.8%; Pred. No. 8.8e+04;
Matches 7; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY 1 UAUGUCUCUCUUCGCC 19
Db 19 TTTTATCTCTCTTCTCC 1

RESULT 13
LOCUS 158747/21 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 38 from patent US 5652350.
ACCESSION 158747
VERSION 158747.1 GI:2477985
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Watanabe,K.A., Ren,W.-Y. and Weil,R.
TITLE Complementary DNA and toxins
JOURNAL Patent: US 5652350-A 38 29-JUL-1997;
FEATURES
source
1..21
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 59.2%; Score 14.2; DB 2; Length 21;
Best Local Similarity 36.8%; Pred. No. 8.8e+04;
Matches 7; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY 1 UAUGUCUCUCUUCGCC 19
Db 19 TTTTATCTCTCTTCTCC 1

RESULT 14
LOCUS AX649750/25 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 1590 from Patent EP1273660.
ACCESSION AX649750
VERSION AX649750.1 GI:29152568
KEYWORDS
```

```
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,Y.
TITLE Human sodium-hydrogen exchanger like protein 1
JOURNAL Patent: EP 1273660-A 1590 08-JAN-2003;
Aeomica, Inc. (US)
FEATURES
source
1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 59.2%; Score 14.2; DB 2; Length 25;
Best Local Similarity 52.6%; Pred. No. 8.9e+04;
Matches 10; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 AUUGUCUCUCUUCGCCA 20
Db 25 ACTGTCTCTCCATTCCTCA 7

RESULT 15
LOCUS AX649751/25 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 1591 from Patent EP1273660.
ACCESSION AX649751
VERSION AX649751.1 GI:29152569
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,Y.
TITLE Human sodium-hydrogen exchanger like protein 1
JOURNAL Patent: EP 1273660-A 1591 08-JAN-2003;
Aeomica, Inc. (US)
FEATURES
source
1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 59.2%; Score 14.2; DB 2; Length 25;
Best Local Similarity 52.6%; Pred. No. 8.9e+04;
Matches 10; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 AUUGUCUCUCUUCGCCA 20
Db 24 ACTGTCTCTCCATTCCTCA 6

Search completed: June 19, 2007, 13:51:04
Job time : 1108 secs
```

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 12:28:50 ; Search time 246 Seconds  
(without alignments)  
721.516 Million cell updates/sec

Title: US-10-604-726A-5136

Perfect score: 24

Sequence: 1 uauugucuccuuugccaccuc 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 4355164

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_200701.\*

1: Geneseqn1980s.\*

2: Geneseqn1990s.\*

3: Geneseqn2000s.\*

4: Geneseqn2001as.\*

5: Geneseqn2001bs.\*

6: Geneseqn2002as.\*

7: Geneseqn2002bs.\*

8: Geneseqn2003as.\*

9: Geneseqn2003bs.\*

10: Geneseqn2003cs.\*

11: Geneseqn2003ds.\*

12: Geneseqn2004as.\*

13: Geneseqn2004bs.\*

14: Geneseqn2005s.\*

15: Geneseqn2006s.\*

16: Geneseqn2007s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	15.8	65.8	24	4	AAD21686 Imperfect
C 2	15.6	65.0	24	2	AAQ44801
C 3	15.6	65.0	24	2	AAQ44806
C 4	15.6	65.0	24	2	AAT99274 Human PUR
C 5	15.6	65.0	24	2	AAV31726 Nucleotid
C 6	15.6	65.0	24	2	AAV31731 Nucleotid
C 7	15.6	65.0	24	2	AAV31731 Nucleotid
C 8	15.6	65.0	24	2	AAV31731 Nucleotid
C 9	15.6	65.0	25	15	AE94315 3' primer
C 10	15.2	63.3	21	7	ADI94591 Murine IF
C 11	15.2	63.3	22	7	ADI94589 Murine IF
C 12	14.4	60.0	18	2	AAQ65826 Type II p
C 13	14.4	60.0	20	7	ADI94593 Murine IF
C 14	14.4	60.0	23	2	AAQ85989 S.tuberos
C 15	14.2	59.2	21	2	AAQ56946 HIV-1 pro
C 16	14.2	59.2	21	15	AEF13105 Human mut
C 17	14.2	59.2	25	10	ADC05103 Human Na/

C 18	14.2	59.2	25	10	ADC05104 Human Na/
C 19	14.2	59.2	25	10	ADC05109 Human Na/
C 20	14.2	59.2	25	10	ADC05105 Human Na/
C 21	14.2	59.2	25	10	ADC05108 Human Na/
C 22	14.2	59.2	25	10	ADC05106 Human Na/
C 23	14.2	59.2	25	10	ADC05107 Human Na/
C 24	14	58.3	24	2	AAQ38850 Sequence
C 25	14	58.3	24	2	AAQ44802 Oligonucl
C 26	14	58.3	24	2	AAT99270 Human PUR
C 27	14	58.3	24	2	AAV31727 Nucleotid
C 28	14	58.3	24	2	AAV31727 Nucleotid
C 29	14	58.3	24	5	AAH48099 Phytochro
C 30	14	58.3	24	14	AEC26021 Human all
C 31	14	58.3	24	14	AEC28387 Human all
C 32	14	58.3	25	9	ACK16088 Human mic
C 33	13.8	57.5	17	10	ADC03597 Human Na/
C 34	13.8	57.5	20	2	AAQ4034 PCR prime
C 35	13.8	57.5	20	8	ABX04519 Human adi
C 36	13.8	57.5	20	10	ADC01938 Human zai
C 37	13.8	57.5	20	10	AAQ59884 ZC13641 o
C 38	13.8	57.5	20	10	ADFI18008 Human zai
C 39	13.8	57.5	20	10	ACD02558 Novel hum
C 40	13.8	57.5	20	12	ADJ96212 Primer 2C
C 41	13.8	57.5	21	12	ADM72676 Human TAS
C 42	13.8	57.5	25	9	ACI35264 Human mic
C 43	13.8	57.5	25	9	ACI37022 Human mic
C 44	13.8	57.5	25	9	ACI92741 Human mic
C 45	13.8	57.5	25	10	ADC05102 Human Na/

#### ALIGNMENTS

##### RESULT 1

AAD21686/c

ID AAD21686 standard; DNA; 24 BP.

XX

AC AAD21686;

XX

DT 28-JAN-2002 (first entry)

XX

DE Imperfect direct repeat #1 of human RPGR exon ORF15 repetitive sequence.

XX

KW Human; mutation; retinitis pigmentosa GTPase regulator; RPGR; genotyping;

XX

KW open reading frame; ORF; X-linked retinitis pigmentosa; XLRP;

XX

KW gene therapy; screening; forensic analysis; ds.

XX

OS Homo sapiens.

XX

PN WO200177380-A2.

XX

PD 18-OCT-2001.

XX

PP 10-APR-2001; 2001WO-GB001622.

XX

PR 10-APR-2000; 2000GB-00008801.

XX

PA (MEDI-) MEDICAL RES COUNCIL.

XX

PI Wright A;

XX

DR WPI; 2001-663057/76.

XX

PT Diagnosing disease or predisposition to disease, associated with disease

XX

PT causing mutations in retinitis pigmentosa GTPase regulator gene by

XX

PT genotyping ORF15 of the gene, and determining presence of mutations.

XX

PS Disclosure; Fig 4E; 100pp; English.

XX

CC The present invention relates to a method for diagnosing disease or

XX

CC predisposition to a disease, associated with a disease causing mutations

XX

CC in a retinitis pigmentosa GTPase regulator (RPGR) gene involves

XX

CC genotyping a RPGR gene, and determining whether the genotype comprises a



```
DT 15-APR-1998 (first entry)
XX Human PUR-alpha gene probe MR0700.
XX
XX PUR element; human; c-myc; inhibitor; hyperproliferative disease; ss;
XX cancer; probe; hybridisation.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX US5672479-A.
XX
XX 30-SEP-1997.
XX
XX 07-JUN-1995; 95US-00486421.
XX
XX 28-AUG-1992; 92US-00938189.
XX
XX 02-FEB-1993; 93US-00014943.
XX
XX 06-JUN-1995; 95US-00470911.
XX
XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
XX Bergemann AD, Johnson EM;
XX
XX WPI; 1997-488859/45.
XX
XX Assays for PUR protein ligands or modulators - using immobilised PUR
XX protein or fragments, to treat hyper-proliferative diseases, e.g. cancer.
XX
XX Example; Col 26; 64pp; English.
XX
XX The probes AAT99270-T99277 were used to screen for positive clones
XX containing a 467 bp Sau3AI fragment of the human c-myc upstream region
XX cloned into pUC19. Isolated sequences were then used as probes to screen
XX an expression library for sequences encoding the PUR protein. The PUR
XX sequence can be used to identify chemical or biological compounds that
XX bind to PUR or binding fragments of PUR. Inhibitors of PUR activity may
XX be used to treat hyperproliferative diseases such as cancer
XX
XX Sequence 24 BP; 2 A; 14 C; 0 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 65.0%; Score 15.6; DB 2; Length 24;
XX Best Local Similarity 50.0%; Pred. No. 4.8e+03;
XX Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
XX
QY 3 UUGUCUCUCUUCGCCACCTC 24
Db ::::: : |||||:
2 TTTTCTCTCCCTCCACCACTC 23

RESULT 5
AAV31726/c
ID. AAV31726 standard; DNA; 24 BP.
XX
XX AAV31726;
XX
XX 24-SEP-1998 (first entry)
XX
XX Nucleotide sequence of the PUR element.
XX
XX PUR-alpha gene; inhibition; viral infection; cancer; PUR element;
XX hyperproliferative disease; ss.
XX
XX Homo sapiens.
XX
XX US5756684-A.
XX
XX 26-MAY-1998.
XX
XX 06-JUN-1995; 95US-00470911.
XX
XX 28-AUG-1992; 92US-00938189.
XX
XX 02-FEB-1993; 93US-00014943.
XX
XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
XX Bergemann AD, Johnson EM;
XX
XX WPI; 1998-321632/28.
XX
XX PUR protein and its fragments - that inhibit PUR protein binding to PUR
XX element or other proteins.
XX
XX Example 6.1.1; Col 27; 63pp; English.
XX
XX This is the nucleotide sequence of an oligonucleotide used in the method
XX of the invention, involving the use of the PUR protein and its fragments,
XX which inhibit PUR protein binding to PUR element or other proteins.
XX
XX Inhibitors of PUR activity may be useful for treating viral infections
XX and hyperproliferative diseases such as cancer
XX
XX Sequence 24 BP; 2 A; 14 C; 0 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 65.0%; Score 15.6; DB 2; Length 24;
XX
QY 3 UUGUCUCUCUUCGCCACCTC 24
Db ::::: : |||||:
2 TTTTCTCTCCCTCCACCACTC 23

RESULT 6
AAV31731
ID. AAV31731 standard; DNA; 24 BP.
XX
XX AAV31731;
XX
XX 24-SEP-1998 (first entry)
XX
XX Nucleotide sequence of the oligonucleotide MR0700.
XX
XX PUR-alpha gene; inhibition; viral infection; cancer; PUR element;
XX hyperproliferative disease; ss.
XX
XX Synthetic.
XX
XX US5756684-A.
XX
XX 26-MAY-1998.
XX
XX 06-JUN-1995; 95US-00470911.
XX
XX 28-AUG-1992; 92US-00938189.
XX
XX 02-FEB-1993; 93US-00014943.
XX
XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
XX Bergemann AD, Johnson EM;
XX
XX WPI; 1998-321632/28.
XX
XX PUR protein and its fragments - that inhibit PUR protein binding to PUR
XX element or other proteins.
XX
XX Example 6.1.1; Col 27; 63pp; English.
XX
XX This is the nucleotide sequence of an oligonucleotide used in the method
XX of the invention, involving the use of the PUR protein and its fragments,
XX which inhibit PUR protein binding to PUR element or other proteins.
XX
XX Inhibitors of PUR activity may be useful for treating viral infections
XX and hyperproliferative diseases such as cancer
XX
XX Sequence 24 BP; 2 A; 14 C; 0 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 65.0%; Score 15.6; DB 2; Length 24;
XX
QY 3 UUGUCUCUCUUCGCCACCTC 24
Db ::::: : |||||:
23 TTTTCTCTCCCTCCACCACTC 2
```

```
XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
XX Bergemann AD, Johnson EM;
XX
XX WPI; 1998-321632/28.
XX
XX PUR protein and its fragments - that inhibit PUR protein binding to PUR
XX element or other proteins.
XX
XX Disclosure; Col 12; 63pp; English.
XX
XX This is the nucleotide sequence of the PUR element used in the method of
XX the invention, involving the use of the PUR protein and its fragments,
XX which inhibit PUR protein binding to PUR element or other proteins.
XX
XX Inhibitors of PUR activity may be useful for treating viral infections
XX and hyperproliferative diseases such as cancer
XX
XX Sequence 24 BP; 8 A; 0 C; 14 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 65.0%; Score 15.6; DB 2; Length 24;
XX Best Local Similarity 50.0%; Pred. No. 4.8e+03;
XX Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
XX
QY 3 UUGUCUCUCUUCGCCACCTC 24
Db ::::: : |||||:
23 TTTTCTCTCCCTCCACCACTC 2

RESULT 6
AAV31731
ID. AAV31731 standard; DNA; 24 BP.
XX
XX AAV31731;
XX
XX 24-SEP-1998 (first entry)
XX
XX Nucleotide sequence of the oligonucleotide MR0700.
XX
XX PUR-alpha gene; inhibition; viral infection; cancer; PUR element;
XX hyperproliferative disease; ss.
XX
XX Synthetic.
XX
XX US5756684-A.
XX
XX 26-MAY-1998.
XX
XX 06-JUN-1995; 95US-00470911.
XX
XX 28-AUG-1992; 92US-00938189.
XX
XX 02-FEB-1993; 93US-00014943.
XX
XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
XX Bergemann AD, Johnson EM;
XX
XX WPI; 1998-321632/28.
XX
XX PUR protein and its fragments - that inhibit PUR protein binding to PUR
XX element or other proteins.
XX
XX Example 6.1.1; Col 27; 63pp; English.
XX
XX This is the nucleotide sequence of an oligonucleotide used in the method
XX of the invention, involving the use of the PUR protein and its fragments,
XX which inhibit PUR protein binding to PUR element or other proteins.
XX
XX Inhibitors of PUR activity may be useful for treating viral infections
XX and hyperproliferative diseases such as cancer
XX
XX Sequence 24 BP; 2 A; 14 C; 0 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 65.0%; Score 15.6; DB 2; Length 24;
XX
QY 3 UUGUCUCUCUUCGCCACCTC 24
Db ::::: : |||||:
23 TTTTCTCTCCCTCCACCACTC 2
```

```

Best Local Similarity 50.0%; Pred. No. 4.8e+03;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 3 UUGUCUCUCUUCGCGCACCC 24
Db 2 TTTTCTCTCCCTCCACCACTC 23

RESULT 7
AAX04070/C
ID AAX04070 standard; DNA; 24 BP.
AC AAX04070;
XX
XX
XX 12-APR-1999. (first entry)
DE Oligonucleotide MF0677 used in PUR identification/characterisation.
XX PUR element; PUR-alpha; hyperproliferative disease; cancer; human;
KW monoclonal antibody; identification; characterisation; ss.
XX Synthetic.
OS Homo sapiens.
XX
XX US5869622-A.
PN
PD
PD 09-FEB-1999.
XX
XX 07-JUN-1995; 95US-00486809.
XX
XX 28-AUG-1992; 92US-00938189.
PR 02-FEB-1993; 93US-00014943.
PR 06-JUN-1995; 95US-00470911.
XX
XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
XX Bergemann AD, Johnson EM;
XX
XX WPI; 1999-152881/13.
XX
XX Monoclonal antibody specific for PUR protein - useful for treating
XX cancer.
XX
XX Example; Col 27; 64pp; English.
XX
XX The present invention describes a monoclonal antibody that specifically
XX binds to an epitope of the PUR protein. Antibodies that bind to the PUR
XX protein and neutralise PUR activity may be used to treat
XX hyperproliferative diseases such as cancer. PUR antibodies may be used
XX diagnostically to detect aberrant expression of the PUR protein and/or
XX mutations in the PUR gene. The present sequence represents an
XX oligonucleotide used in the identification and characterisation of the
XX PUR protein and its sequence element PUR repeat, in an example from the
XX present invention
XX
XX Sequence 24 BP; 8 A; 0 C; 14 G; 2 T; 0 U; 0 Other;

Query Match 65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 4.8e+03;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 3 UUGUCUCUCUUCGCGCACCC 24
Db 23 TTTTCTCTCCCTCCACCACTC 2

RESULT 8
AAX04075
ID AAX04075 standard; DNA; 24 BP.
XX
XX
XX AAX04075;
AC
XX
XX 12-APR-1999 (first entry)
DE
DE
DE 3' primer for PCR of DNase I treated OLIG2 chromatin.
XX
XX chromatin; DNA hybridization; DNA amplification; DNA microarray;
KW diagnosis; ss; primer; PCR; OLIG2.
XX
XX Homo sapiens.
XX
XX WO2005118873-A2.
XX
XX
XX 15-DEC-2005.
PD
XX
XX 31-MAY-2005; 2005WO-US019150.
PF
XX
XX 28-MAY-2004; 2004US-0575478P.
PR

```

```

XX Oligonucleotide MR0700 used in PUR identification/characterisation.
DE
XX
XX PUR element; PUR-alpha; hyperproliferative disease; cancer; human;
KW monoclonal antibody; identification; characterisation; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX US5869622-A.
PN
PD
PD 09-FEB-1999.
XX
XX 07-JUN-1995; 95US-00486809.
XX
XX 28-AUG-1992; 92US-00938189.
PR 02-FEB-1993; 93US-00014943.
PR 06-JUN-1995; 95US-00470911.
XX
XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
XX Bergemann AD, Johnson EM;
XX
XX WPI; 1999-152881/13.
XX
XX Monoclonal antibody specific for PUR protein - useful for treating
XX cancer.
XX
XX Example; Col 27; 64pp; English.
XX
XX The present invention describes a monoclonal antibody that specifically
XX binds to an epitope of the PUR protein. Antibodies that bind to the PUR
XX protein and neutralise PUR activity may be used to treat
XX hyperproliferative diseases such as cancer. PUR antibodies may be used
XX diagnostically to detect aberrant expression of the PUR protein and/or
XX mutations in the PUR gene. The present sequence represents an
XX oligonucleotide used in the identification and characterisation of the
XX PUR protein and its sequence element PUR repeat, in an example from the
XX present invention
XX
XX Sequence 24 BP; 2 A; 14 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 65.0%; Score 15.6; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 4.8e+03;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 3 UUGUCUCUCUUCGCGCACCC 24
Db 2 TTTTCTCTCCCTCCACCACTC 23

RESULT 9
AEE94315/C
ID AEE94315 standard; DNA; 25 BP.
XX
XX
XX AEE94315;
AC
XX
XX 23-FEB-2006 (first entry)
DT
DT
DT 3' primer for PCR of DNase I treated OLIG2 chromatin.
XX
XX chromatin; DNA hybridization; DNA amplification; DNA microarray;
KW diagnosis; ss; primer; PCR; OLIG2.
XX
XX Homo sapiens.
XX
XX WO2005118873-A2.
XX
XX
XX 15-DEC-2005.
PD
XX
XX 31-MAY-2005; 2005WO-US019150.
PF
XX
XX 28-MAY-2004; 2004US-0575478P.
PR

```



XX functional domain; nucleic acid cleavage assay; nuclease; polymerase;  
 KW detection; microorganism; RNA genome; hepatitis C;  
 KW human immunodeficiency virus; ss; probe.  
 OS Mus musculus.  
 XX  
 PN W0200190337-A2.  
 XX  
 XX 29-NOV-2001.  
 PD  
 XX  
 XX 24-MAY-2001; 2001WO-US017086.  
 XX  
 XX 24-MAY-2000; 2000US-00577304.  
 PR  
 PR 11-JAN-2001; 2001US-00758282.  
 PR  
 PR 24-MAY-2001; 2001US-00864426.  
 PR  
 PR 24-MAY-2001; 2001US-00864636.  
 XX  
 XX (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 PA  
 XX Allawi H, Bartholomay CT, Chehak L, Curtis ML, Eis PS, Hall JG;  
 XX Ip HS, Kaiser M, Kwiatkowski RW, Lukowski AA, Lymanichev V, Ma W;  
 XX Olson-Muncz MC, Olson SM, Schaefer JJ, Skrzypczynski Z, Takova TY;  
 XX Vedvik KL, Lymanichev NE, Neri BP;  
 XX  
 XX WPI; 2002-083110/11.  
 XX  
 XX Composition comprising enzyme which comprises heterologous functional  
 XX domain that provides altered functionality in nucleic acid cleavage  
 XX assay, useful for cleaving nucleic acid, and detecting presence of RNA  
 XX target.  
 XX  
 XX Claim 95; SEQ ID NO 2142; 1266pp; English.  
 PS  
 XX This invention describes a novel composition comprising an enzyme which  
 XX contains a heterologous functional domain that provides altered  
 XX functionality in a nucleic acid cleavage assay. The enzyme comprises a 5'  
 XX nuclease, preferably a thermostable 5' nuclease, or a polymerase which is  
 XX altered in sequence related to a naturally occurring sequence of a  
 XX polymerase such that it exhibits reduced DNA synthetic activity from that  
 XX of the naturally occurring polymerase. Preferably the polymerase is a  
 XX thermostable polymerase from a Thermus species such as T. aquaticus, T.  
 XX flavus, T. thermophilus, T. filiformis or T. scotoductus. The enzyme  
 XX comprises a heterologous functional domain, an amino acid sequence that  
 XX provides an improved substrate binding activity in the nucleic acid  
 XX cleavage assay and an amino acid sequence that provides improved  
 XX background specificity in the nucleic acid cleavage assay. The invasive  
 XX cleavage structure comprises a RNA target nucleic acid (a cytochrome  
 XX P450, or cytokine RNA). Cleavage of the invasive cleavage structure  
 XX generates an non-target cleavage product, which is then detected by  
 XX detecting fluorescence, mass or fluorescence energy transfer or by  
 XX detecting radioactivity luminescence, phosphorescence, fluorescence  
 XX polarisation or charge. The enzyme is useful for cleaving a nucleic acid  
 XX which involves exposing a sample (a cell lysate) comprising substrate  
 XX nucleic acid to the enzyme which produces at least one detectable  
 XX cleavage product. The enzyme is employed for detecting target DNAs and  
 XX RNAs comprising wild-type and mutant alleles of genes including genes  
 XX from humans, other animal or plants that are or may be associated with  
 XX disease or other conditions. In addition, the enzymes may be useful for  
 XX detecting and identifying strains of microorganisms including bacteria,  
 XX fungi, protozoa, ciliates and viruses, preferably detecting and  
 XX identifying viruses having RNA genomes, such as hepatitis C and human  
 XX immunodeficiency virus.  
 XX  
 XX Sequence 22 BP; 9 A; 3 C; 9 G; 1 T; 0 U; 0 Other;  
 SQ  
 Query Match 63.3%; Score 15.2; DB 7; Length 22;  
 Best Local Similarity 50.0%; Pred. No. 7.1e+03;  
 Matches 10; Conservative 7; Mismatches 3; Indels 0; Gaps 0;  
 OY 5 GUCUCUCCUUGCCACUCC 24  
 DB 21 GTCCTCTCTTTCGCCAGTTC 2

RESULT 12  
 AAQ65826  
 ID AAQ65826 standard; DNA; 18 BP.  
 XX  
 AC AAQ65826;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 20-DEC-1994 (first entry)  
 XX  
 XX Type II procollagen sequencing primer 96.  
 DE  
 XX Type II procollagen; COL2A1; amplification; primer;  
 KW polymerase chain reaction; PCR; osteoarthritis; cartilage; ss.  
 KW  
 XX Synthetic.  
 OS  
 XX W09411532-A1.  
 PN  
 XX 26-MAY-1994.  
 PD  
 XX 12-NOV-1993; 93WO-US010964.  
 PF  
 XX 13-NOV-1992; 92US-00977284.  
 PR  
 XX (UWJE-) UNIV JEFFERSON THOMAS.  
 XX  
 XX Prockop DJ, Ala-Kokko L, Williams CJ, Ritvaniemi P, Baldwin C;  
 PI Hopkinson I, Ahmad NN;  
 PI  
 XX WPI; 1994-183530/22.  
 DR  
 XX Detecting genetic pre-disposition to osteoarthritis - and other diseases  
 XX involving mutation in cartilage protein genes, by amplification and  
 XX analysis of DNA and comparison with standards.  
 XX  
 XX Claim 18; Page 26; 112pp; English.  
 PS  
 XX Claim 18 claims primers for use in detecting mutations in a mammalian  
 XX gene for a structural protein of cartilage comprising a sequence  
 XX identified in Table 1 (Page 18-31). Table 1 includes 179 primer sequences  
 XX (see AAQ65728-Q65906). The following details are given for primer 96:  
 XX Region/exon: 31 Direction: sense Primer position: 12824 (Updated on 25-  
 XX MAR-2003 to correct PN field.)  
 CC  
 XX Sequence 18 BP; 1 A; 10 C; 1 G; 6 T; 0 U; 0 Other;  
 SQ  
 Query Match 60.0%; Score 14.4; DB 2; Length 18;  
 Best Local Similarity 62.5%; Pred. No. 1.5e+04;  
 Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
 OY 9 CUUUUUUCCUCCACUCC 24  
 DB 3 CTCCTTTCCTCCACCTC 18  
 RESULT 13  
 ADI94593/c  
 ID ADI94593 standard; DNA; 20 BP.  
 XX  
 AC ADI94593;  
 XX  
 XX 04-NOV-2004 (first entry)  
 DT  
 XX Murine IFN-gamma associated probe SEQ ID 2146.  
 DE  
 XX functional domain; nucleic acid cleavage assay; nuclease; polymerase;  
 KW detection; microorganism; RNA genome; hepatitis C;  
 KW human immunodeficiency virus; ss; probe.  
 XX  
 OS Mus musculus.  
 XX



PN WO200190337-A2.  
XX  
PD 29-NOV-2001.  
XX  
PF 24-MAY-2001; 2001WO-US017086.  
XX  
XX 24-MAY-2000; 2000US-00577304.  
PR 11-JAN-2001; 2001US-00758282.  
PR 24-MAY-2001; 2001US-00864426.  
PR 24-MAY-2001; 2001US-00864636.  
XX  
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.  
PA  
XX Allawi H, Bartholomay CT, Chehak L, Curtis ML, Eis PS, Hall JG;  
PI Ip HS, Kaiser M, Kwiatkowski RW, Lukowiak AA, Lyamichev V, Ma W;  
PI Olson-Munoz MC, Olson SM, Schaefer JJ, Skrzypczynski Z, Takova TV;  
PI Vedvik KL, Lyamichev NE, Neri BP;  
XX WPI; 2002-083110/11.  
DR  
XX Composition comprising enzyme which comprises heterologous functional  
XX domain that provides altered functionality in nucleic acid cleavage  
PT assay, useful for cleaving nucleic acid, and detecting presence of RNA  
PT target.  
PT  
XX Claim 95; SEQ ID NO 2146; 1266pp; English.  
PS  
XX This invention describes a novel composition comprising an enzyme which  
CC contains a heterologous functional domain that provides altered  
CC functionality in a nucleic acid cleavage assay. The enzyme comprises a 5'  
CC nuclease, preferably a thermostable 5' nuclease, or a polymerase which is  
CC altered in sequence related to a naturally occurring sequence of a  
CC polymerase such that it exhibits reduced DNA synthetic activity from that  
CC of the naturally occurring polymerase. Preferably the polymerase is a  
CC thermostable polymerase from a Thermus species such as T. aquaticus, T.  
CC flavus, T. thermophilus, T. filiformis or T. scotoductus. The enzyme  
CC comprises a heterologous functional domain, an amino acid sequence that  
CC provides an improved substrate binding activity in the nucleic acid  
CC cleavage assay and an amino acid sequence that provides improved  
CC background specificity in the nucleic acid cleavage assay. The invasive  
CC cleavage structure comprises a RNA target nucleic acid (a cytochrome  
CC P450, or cytokine RNA). Cleavage of the invasive cleavage structure  
CC generates a non-target cleavage product, which is then detected by  
CC detecting fluorescence, mass or fluorescence energy transfer or by  
CC detecting radioactivity luminescence, phosphorescence, fluorescence  
CC polarisation or charge. The enzyme is useful for cleaving a nucleic acid  
CC which involves exposing a sample (a cell lysate) comprising substrate  
CC nucleic acid to the enzyme which produces at least one detectable  
CC cleavage product. The enzyme is employed for detecting target DNAs and  
CC RNAs comprising wild-type and mutant alleles of genes including genes  
CC from humans, other animal or plants that are or may be associated with  
CC disease or other conditions. In addition, the enzymes may be useful for  
CC detecting and identifying strains of microorganisms including bacteria,  
CC fungi, protozoa, ciliates and viruses, preferably detecting and  
CC identifying viruses having RNA genomes, such as hepatitis C and human  
XX immunodeficiency virus.  
XX  
SQ Sequence 20 BP; 9 A; 3 C; 7 G; 1 T; 0 U; 0 Other;  
Query Match 60.0%; Score 14.4; DB 7; Length 20;  
Best Local Similarity 56.2%; Pred. No. 1.5e+04;  
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
QY 5 GUCUCUCCUUUCGCCA 20  
Db 19 GTCTCTCTTTGCCA 4  
RESULT 14  
AAQ85989/c  
ID AAQ85989 standard; DNA; 23 BP.  
XX  
AC AAQ85989;  
Query Match 60.0%; Score 14.4; DB 2; Length 23;  
Best Local Similarity 56.2%; Pred. No. 1.6e+04;  
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
QY 8 UCUCUUUCGCCACCU 23  
Db 20 TCTCTCTTTGCCACCT 5  
RESULT 15  
AAQ56946/c  
ID AAQ56946 standard; DNA; 21 BP.  
XX  
AC AAQ56946;  
XX  
DT 16-OCT-2003 (revised)  
DT 15-JUL-1999 (first entry)  
XX  
XX HIV-1 proviral DNA fragment 29.  
XX  
XX DNA-targeting conjugate; anticancer drug; viral DNA-cleaving agent;  
XX viral DNA-binding agent; solid support; primer; ss.  
XX  
XX Human immunodeficiency virus 1.  
XX  
PN WO9531434-A1.

XX  
DT 25-MAR-2003 (revised)  
DT 12-OCT-1995 (first entry)  
XX  
XX S.tuberosum PFK probe PFK23.  
XX  
XX ATP-dependent fructose-6-phosphate 1-phosphotransferase enzyme; plant;  
KW potato; Solanum tuberosum; rice; Oryza sativa; maize; Zea mays; radish;  
KW Raphanus sativus; Flaveria brownii; primer; expression vector; probe;  
KW Agrobacterium tumefaciens; sugar; storage; temperature; ss.  
XX  
OS Synthetic.  
XX  
XX WO9505457-A1.  
XX  
XX 23-FEB-1995.  
XX  
XX 16-AUG-1994; 94WO-JP001352.  
XX  
XX 19-AUG-1993; 93JP-00226454.  
XX  
XX (NISB ) JAPAN TOBACCO INC.  
XX  
XX Hiroyoshi T, Mine T, Kasaoka K, Tyson HR, Page MJA;  
XX  
XX WPI; 1995-098757/13.  
XX  
XX DNA coding for fructose-6-phosphate 1-phosphotransferase - of plant  
XX origin, for prodn. of transformant plant cells with altered sugar  
XX content.  
XX  
XX Example 7; Page 15; 79pp; Japanese.  
XX  
XX The sequence of the probe PFK23 derived from a 60 bp amplified fragment  
XX encoding an N-terminal peptide (AAR71610) from the novel potato (Solanum  
XX tuberosum) ATP-dependent fructose-6-phosphate 1-phosphotransferase enzyme  
XX (EC 2.7.1.11; PFK). The probe was used to obtain 11 clones of the PFK  
XX gene. These clones, amplified by PCR using the primers (AAQ85990-3),  
XX ligated into the plasmid pBluescript SKII(-). The full length gene  
XX (AAQ85982) was used to generate the expression vector pPFK(35S) which was  
XX transformed into plants via Agrobacterium tumefaciens. Transformed plants  
XX expressing the enzyme can be used to produce varieties that have altered  
XX sugar content on storage at low temperatures. (Updated on 25-MAR-2003 to  
XX correct PN field.)  
XX  
SQ Sequence 23 BP; 9 A; 0 C; 9 G; 5 T; 0 U; 0 Other;  
Query Match 60.0%; Score 14.4; DB 2; Length 23;  
Best Local Similarity 56.2%; Pred. No. 1.6e+04;  
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
QY 8 UCUCUUUCGCCACCU 23  
Db 20 TCTCTCTTTGCCACCT 5



GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 12:53:27 ; Search time 256 Seconds  
(without alignments)  
175.760 Million cell updates/sec

Title: US-10-604-726A-5136

Perfect score: 24

Sequence: 1 uauugucucuccuucgcaccuc 24

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 960512

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1 COMB.seq\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5 COMB.seq\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A COMB.seq\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B COMB.seq\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7 COMB.seq\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H COMB.seq\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS COMB.seq\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP COMB.seq\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE COMB.seq\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15.6	65.0	24	2	US-08-014-943A-3
C 2	15.6	65.0	24	2	US-08-014-943A-15
C 3	15.6	65.0	24	2	US-08-486-421-20
C 4	15.6	65.0	24	2	US-08-486-421-38
C 5	15.6	65.0	24	2	US-08-470-911-20
C 6	15.6	65.0	24	2	US-08-470-911-38
C 7	15.6	65.0	24	2	US-08-486-809-20
C 8	15.6	65.0	24	2	US-08-486-809-38
C 9	14.4	60.0	18	2	US-07-977-284A-99
C 10	14.4	60.0	18	2	US-08-256-426B-99
C 11	14.2	59.2	21	2	US-08-242-664-38
C 12	14.2	59.2	21	2	US-08-484-138-38
C 13	14.2	59.2	21	7	PCT-US95-06379-38
C 14	14	58.3	24	2	US-08-014-943A-12
C 15	14	58.3	24	2	US-08-486-421-34
C 16	14	58.3	24	2	US-08-470-911-34
C 17	14	58.3	24	2	US-08-486-809-34
C 18	14	58.3	25	3	US-09-396-196G-81941
C 19	13.8	57.5	20	3	US-09-118-408-10
C 20	13.8	57.5	20	3	US-09-506-855-10
C 21	13.8	57.5	20	3	US-09-911-176B-10
C 22	13.8	57.5	20	3	US-09-619-740-10
C 23	13.8	57.5	20	3	US-09-198-452A-3360

C 24	13.8	57.5	20	3	US-09-506-852-10	Sequence 10, Appl
C 25	13.8	57.5	20	3	US-10-392-706-10	Sequence 10, Appl
C 26	13.6	56.7	25	3	US-09-396-196G-64399	Sequence 64399, A
C 27	13.6	56.7	25	3	US-09-396-196G-119671	Sequence 119671, A
C 28	13.4	55.8	17	2	US-07-977-284A-100	Sequence 100, Appl
C 29	13.4	55.8	17	2	US-08-256-426B-100	Sequence 100, Appl
C 30	13.4	55.8	24	3	US-08-445-463B-56	Sequence 56, Appl
C 31	13.4	55.8	24	3	US-08-445-463B-57	Sequence 57, Appl
C 32	13.4	55.8	24	3	US-08-445-464C-56	Sequence 56, Appl
C 33	13.4	55.8	24	3	US-08-445-464C-57	Sequence 57, Appl
C 34	13.4	55.8	24	3	US-08-044-857D-56	Sequence 56, Appl
C 35	13.4	55.8	24	3	US-08-044-857D-57	Sequence 57, Appl
C 36	13.4	55.8	24	7	PCT-US94-03437-56	Sequence 56, Appl
C 37	13.4	55.8	24	7	PCT-US94-03437-57	Sequence 57, Appl
C 38	13.4	55.8	25	3	US-09-543-771B-365	Sequence 365, App
C 39	13.4	55.8	25	3	US-09-543-771B-365	Sequence 365, App
C 40	13.4	55.8	25	3	US-09-396-196G-14417	Sequence 14417, A
C 41	13.4	55.8	25	3	US-09-396-196G-14428	Sequence 14428, A
C 42	13.4	55.8	25	3	US-09-396-196G-57430	Sequence 57430, A
C 43	13.4	55.8	25	3	US-09-396-196G-117149	Sequence 117149, A
C 44	13.2	55.0	20	3	US-09-265-630-15	Sequence 15, Appl
C 45	13.2	55.0	21	3	US-08-983-605-322	Sequence 322, App

## ALIGNMENTS

RESULT 1  
US-08-014-943A-3/C  
; Sequence 3, Application US/08014943A  
; Patent No. 5545551  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Edward M.  
; APPLICANT: Bergemann, Andrew D.  
; TITLE OF INVENTION: Cloning And Expression Of PUR Protein  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/014,943A  
; FILING DATE: 02/FEB/1992  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 6923-033  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 790-9090  
; TELEFAX: 212 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 24 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
US-08-014-943A-3

Query Match 65.0%; Score 15.6; DB 2; Length 24;  
Best Local Similarity 50.0%; Pred. No. 6.4e+02;  
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 3 UUGUCUCUCUUCGCCACCUC 24  
Db 23 TTTTCTCTCCTCCACCCTC 2

## RESULT 2

US-08-014-943A-15  
Sequence 15, Application US/08014943A  
Patent No. 5545551  
GENERAL INFORMATION:  
APPLICANT: Johnson, Edward M.  
APPLICANT: Bergemann, Andrew D.  
TITLE OF INVENTION: Cloning And Expression Of PUR Protein  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/014,943A  
FILING DATE: 02/FEB/1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 6923-033  
TELEPHONE: 212 790-9090  
TELEFAX: 212 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-08-014-943A-15

Query Match 65.0%; Score 15.6; DB 2; Length 24;  
Best Local Similarity 50.0%; Pred. No. 6.4e+02;  
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 3 UUGUCUCUCUUCGCCACCUC 24  
Db 2 TTTTCTCTCCTCCACCCTC 23

## RESULT 3

US-08-486-421-20/c  
Sequence 20, Application US/08486421  
Patent No. 5672479  
GENERAL INFORMATION:  
APPLICANT: Johnson, Edward M.  
APPLICANT: Bergemann, Andrew D.  
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,421  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470,911  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 6923-053  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-08-486-421-20

Query Match 65.0%; Score 15.6; DB 2; Length 24;  
Best Local Similarity 50.0%; Pred. No. 6.4e+02;  
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 3 UUGUCUCUCUUCGCCACCUC 24  
Db 23 TTTTCTCTCCTCCACCCTC 2

## RESULT 4

US-08-486-421-38  
Sequence 38, Application US/08486421  
Patent No. 5672479  
GENERAL INFORMATION:  
APPLICANT: Johnson, Edward M.  
APPLICANT: Bergemann, Andrew D.  
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,421  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470,911  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 6923-053  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 38:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 24 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

US-08-486-421-38

Query Match 65.0%; Score 15.6; DB 2; Length 24;

Best Local Similarity 50.0%; Pred. No. 6.4e+02;

Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Oy 3 UUGUCUCUCCUUGGCCACCTC 24

Db 2 TTTTCTCTCCCTCCACCACTC 23

RESULT 5

US-08-470-911-20/c

; Sequence 20, Application US/08470911

; Patent No. 5756684

; GENERAL INFORMATION:

; APPLICANT: Johnson, Edward M.

; APPLICANT: Bergemann, Andrew D.

; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN

; NUMBER OF SEQUENCES: 51

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/470,911

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 6923-053

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 20:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 24 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: unknown

; MOLECULE TYPE: DNA (genomic)

US-08-470-911-20

Query Match 65.0%; Score 15.6; DB 2; Length 24;

Best Local Similarity 50.0%; Pred. No. 6.4e+02;

Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Oy 3 UUGUCUCUCCUUGGCCACCTC 24

Db 23 TTTTCTCTCCCTCCACCACTC 2

RESULT 6

US-08-470-911-38

; Sequence 38, Application US/08470911

; Patent No. 5756684

; GENERAL INFORMATION:

; APPLICANT: Johnson, Edward M.

; APPLICANT: Bergemann, Andrew D.

; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN

; NUMBER OF SEQUENCES: 51

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/470,911

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 6923-053

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 38:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 24 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

US-08-470-911-38

Query Match

Best Local Similarity 50.0%; Score 15.6; DB 2; Length 24;

Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Oy 3 UUGUCUCUCCUUGGCCACCTC 24

Db 2 TTTTCTCTCCCTCCACCACTC 23

RESULT 7

US-08-486-809-20/c

; Sequence 20, Application US/08486809

; Patent No. 5869622

; GENERAL INFORMATION:

; APPLICANT: Johnson, Edward M.

; APPLICANT: Bergemann, Andrew D.

; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN

; NUMBER OF SEQUENCES: 51

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/486,809

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/470,911  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 6923-053  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-08-486-809-20

Query Match 65.0%; Score 15.6; DB 2; Length 24;  
Best Local Similarity 50.0%; Pred. NO. 6.4e+02;  
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 3 UUGUCUCUCCUUUGCCACCC 24  
Db 23 TTTTCTCTCCCTCCACCCCTC 2

RESULT 8  
US-08-486-809-38  
Sequence 38, Application US/08486809  
Patent No. 5869622  
GENERAL INFORMATION:  
APPLICANT: Johnson, Edward M.  
APPLICANT: Bergemann, Andrew D.  
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,809  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470,911  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 6923-053  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-486-809-38

Query Match 65.0%; Score 15.6; DB 2; Length 24;  
Best Local Similarity 50.0%; Pred. NO. 6.4e+02;  
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 3 UUGUCUCUCCUUUGCCACCC 24  
Db 2 TTTTCTCTCCCTCCACCCCTC 23

RESULT 9  
US-07-977-284A-99  
Sequence 99, Application US/07977284A  
Patent No. 5558988  
GENERAL INFORMATION:  
APPLICANT: Prockop, Darwin J.  
APPLICANT: Ala-Kokko, Leena  
APPLICANT: Williams, Charlene J.  
APPLICANT: Ritvaniemi, Pertti  
APPLICANT: Baldwin, Clinton  
APPLICANT: Hopkinson, Ian  
APPLICANT: Ahmad, Nilofer Nina  
TITLE OF INVENTION: METHODS OF DETECTING A GENETIC  
TITLE OF INVENTION: PREDISPOSITION FOR OSTEOARTHRITIS  
NUMBER OF SEQUENCES: 261  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5558988ris  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/977,284A  
FILING DATE: 13-NOV-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: TJU-0697  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 99:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
ANTI-SENSE: NO  
US-07-977-284A-99

Query Match 60.0%; Score 14.4; DB 2; Length 18;  
Best Local Similarity 62.5%; Pred. NO. 2.1e+03;  
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CUCCUUUGCCACCC 24  
Db 3 CTCCTTTCCACCCCTC 18

RESULT 10  
US-08-256-426B-99  
Sequence 99, Application US/08256426B  
Patent No. 5948611  
GENERAL INFORMATION:

APPLICANT: Prockop, Darwin J.  
APPLICANT: Ala-Kokko, Leena  
APPLICANT: Williams, Charlene J.  
APPLICANT: Ritvaniemi, Pertti  
APPLICANT: Baldwin, Clinton  
APPLICANT: Hopkinson, Ian  
APPLICANT: Ahmad, Nilofer Nina  
TITLE OF INVENTION: Methods of Detecting A Genetic  
NUMBER OF SEQUENCES: 293  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5948611ris  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 3.1  
SOFTWARE: WORDPERFECT 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,426B  
FILING DATE: 03-FEB-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10964  
FILING DATE: 12-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/977,284  
FILING DATE: 13-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Mark Deluca  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: TJU-1082  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 99:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
ANTI-SENSE: NO  
US-08-256-426B-99

Query Match 60.0%; Score 14.4; DB 2; Length 18;  
Best Local Similarity 62.5%; Pred. No. 2.1e+03;  
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 9 CUUUUUGCCACUC 24  
Db 3 CTCCTTCCACCTC 18

RESULT 11  
US-08-242-664-38/c  
Sequence 38, Application US/08242664  
Patent No. 5571937  
GENERAL INFORMATION:  
APPLICANT: Watanabe, Kyoichi A.  
APPLICANT: Ren, Wu-Yun  
APPLICANT: Weil, Roger  
TITLE OF INVENTION: Complementary DNA and Toxins  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10112

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch 1.44Mb  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/242,664  
FILING DATE: May 12, 1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 44683--Z/JPW/MJG  
TELEPHONE: 212-977-9550  
TELEFAX: 212-664-0525  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

US-08-242-664-38

Query Match 59.2%; Score 14.2; DB 2; Length 21;  
Best Local Similarity 36.8%; Pred. No. 2.7e+03;  
Matches 7; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY 1 UAUGUCUCUUCUUGGCC 19  
Db 19 TTTATCTCTCTTCTCC 1

RESULT 12  
US-08-484-138-38/c  
Sequence 38, Application US/08484138  
Patent No. 5652350  
GENERAL INFORMATION:  
APPLICANT: Watanabe, Kyoichi A.  
APPLICANT: Ren, Wu-Yun  
APPLICANT: Weil, Roger  
TITLE OF INVENTION: Complementary DNA and Toxins  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch 1.44Mb  
COMPUTER: IBM PC  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,138  
FILING DATE: June 7, 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 44683--Z/JPW/MJG  
TELEPHONE: 212-977-9550  
TELEFAX: 212-664-0525  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)  
US-08-484-138-38  
Query Match 59.2%; Score 14.2; DB 2; Length 21;  
Best Local Similarity 36.8%; Pred. No. 2.7e+03;  
Matches 7; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

Qy 1 UAUGUCUCUCUCCUUGGCC 19  
Db 19 TTTTATCTCTCTTCTCC 1

RESULT 13  
PCT-US95-06379-38/c  
Sequence 38, Application PC/TUS9506379  
GENERAL INFORMATION:  
APPLICANT: Watanabe, Kyoichi A.  
APPLICANT: Ren, Wu-Yun  
APPLICANT: Weil, Roger  
TITLE OF INVENTION: Complementary DNA and Toxins  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch 1.44Mb  
COMPUTER: IBM PC  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/06379  
FILING DATE: May 13, 1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 44683-PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0526  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
PCT-US95-06379-38  
Query Match 59.2%; Score 14.2; DB 7; Length 21;  
Best Local Similarity 36.8%; Pred. No. 2.7e+03;  
Matches 7; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

Qy 1 UAUGUCUCUCUCCUUGGCC 19  
Db 19 TTTTATCTCTCTTCTCC 1

RESULT 14  
US-08-014-943A-12/c  
Sequence 12, Application US/08014943A  
Patent No. 5545551  
GENERAL INFORMATION:  
APPLICANT: Johnson, Edward M.  
APPLICANT: Bergemann, Andrew D.  
TITLE OF INVENTION: Cloning And Expression Of Pur Protein  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/014,943A  
FILING DATE: 02/FEB/1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 6923-033  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 790-9090  
TELEFAX: 212 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-08-014-943A-12  
Query Match 58.3%; Score 14; DB 2; Length 24;  
Best Local Similarity 40.9%; Pred. No. 3.4e+03;  
Matches 9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 3 UUGUCUCUCUCCUUGGCCUCC 24  
Db 23 TTTTCTCTTTTCCACCCTC 2

RESULT 15  
US-08-486-421-34/c  
Sequence 34, Application US/08486421  
Patent No. 5672479  
GENERAL INFORMATION:  
APPLICANT: Johnson, Edward M.  
APPLICANT: Bergemann, Andrew D.  
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,421  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470,911  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 6923-053  
TELECOMMUNICATION INFORMATION:



```

; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 34:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 24 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: DNA
;   US-08-486-421-34

Query Match      58.3%; Score 14; DB 2; Length 24;
Best Local Similarity 40.9%; Pred. No. 3.4e+03;
Matches 9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy      3 UUGUCUCUCUUCUUGCCACCTC 24
Db      23 TTTCCTCTTTTCCACCACTC 2

```

Search completed: June 19, 2007, 13:10:06  
 Job time : 255.5 secs

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 13:01:01 ; Search time 1262 Seconds  
(without alignments)  
233.679 Million cell updates/sec

Title: US-10-604-726a-5136

Perfect score: 24

Sequence: 1 uauugucuccuucgcccacc 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 22906428

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA Main:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*  
9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*  
10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*  
11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*  
12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*  
13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10H\_PUBCOMB.seq.\*  
14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10I\_PUBCOMB.seq.\*  
15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10J\_PUBCOMB.seq.\*  
16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10K\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	16.2	67.5	25	16	US-11-136-527-336045
c 2	16	66.7	25	9	US-10-719-900-980988
c 3	16	66.7	25	10	US-10-956-157-42579
c 4	16	66.7	25	10	US-10-956-157-88871
c 5	16	66.7	25	10	US-10-956-157-88877
c 6	16	66.7	25	13	US-11-060-756-47774
c 7	16	66.7	25	13	US-11-060-756-47788
c 8	15.8	65.8	24	11	US-10-310-914A-205339
c 9	15.8	65.8	25	16	US-11-136-527-276878
c 10	15.8	65.8	25	16	US-11-136-527-276903
c 11	15.6	65.0	25	9	US-10-719-900-678730
c 12	15.6	65.0	25	13	US-11-036-317-35846
c 13	15.4	64.2	20	11	US-10-310-914A-498782
c 14	15.4	64.2	25	10	US-10-956-157-21624
c 15	15.4	64.2	25	10	US-10-956-157-21630
c 16	15.4	64.2	25	10	US-10-956-157-21634
c 17	15.4	64.2	25	10	US-10-956-157-21637

c 18	15.2	63.3	21	3	US-09-864-636A-2144	Sequence 2144, Ap
c 19	15.2	63.3	21	3	US-09-864-636A-2144	Sequence 2144, Ap
c 20	15.2	63.3	21	7	US-10-084-833-2144	Sequence 2144, Ap
c 21	15.2	63.3	22	3	US-09-864-636A-2142	Sequence 2142, Ap
c 22	15.2	63.3	22	3	US-09-864-636A-2142	Sequence 2142, Ap
c 23	15.2	63.3	22	7	US-10-084-833-2142	Sequence 2142, Ap
c 24	15	62.5	19	14	US-11-083-784-661177	Sequence 661177,
c 25	15	62.5	19	15	US-11-101-244-661177	Sequence 661177,
c 26	15	62.5	25	10	US-10-956-157-42396	Sequence 42396, A
c 27	15	62.5	25	10	US-10-956-157-42570	Sequence 42570, A
c 28	15	62.5	25	10	US-10-956-157-43354	Sequence 43354, A
c 29	15	62.5	25	10	US-10-956-157-43356	Sequence 43356, A
c 30	15	62.5	25	10	US-10-956-157-43359	Sequence 43359, A
c 31	15	62.5	25	10	US-10-956-157-88872	Sequence 88872, A
c 32	15	62.5	25	13	US-11-060-756-47765	Sequence 47765, A
c 33	15	62.5	25	15	US-11-121-849-524825	Sequence 524825,
c 34	15	62.5	25	16	US-11-136-527-116930	Sequence 116930,
c 35	14.8	61.7	20	11	US-10-310-914A-949541	Sequence 949541,
c 36	14.8	61.7	21	11	US-10-310-914A-426363	Sequence 426363,
c 37	14.8	61.7	24	11	US-10-310-914A-67315	Sequence 67315, A
c 38	14.8	61.7	24	11	US-10-310-914A-144888	Sequence 144888,
c 39	14.8	61.7	24	11	US-10-310-914A-550631	Sequence 550631,
c 40	14.8	61.7	25	8	US-10-719-956-695018	Sequence 695018,
c 41	14.8	61.7	25	11	US-10-933-982-217334	Sequence 217334,
c 42	14.8	61.7	25	13	US-11-036-317-720298	Sequence 720298,
c 43	14.8	61.7	25	15	US-11-121-849-538357	Sequence 538357,
c 44	14.8	61.7	25	16	US-11-136-527-276882	Sequence 276882,
c 45	14.6	60.8	21	11	US-10-310-914A-1070230	Sequence 1070230,

#### ALIGNMENTS

##### RESULT 1

US-11-136-527-336045/c

; Sequence 336045, Application US/11136527

; Publication No. US20050287570A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William M

; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

; FILE REFERENCE: 031896-041000 (AM101086)

; CURRENT APPLICATION NUMBER: US/11/136,527

; PRIORITY FILING DATE: 2005-05-25

; PRIOR APPLICATION NUMBER: US 60/574,294

; PRIOR FILING DATE: 2005-05-26

; NUMBER OF SEQ ID NOS: 362830

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 336045

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: Probe

US-11-136-527-336045

Query Match 67.5%; Score 16.2; DB 16; Length 25;

Best Local Similarity 52.4%; Pred. No. 3.7e+03;

Matches 11; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AUUGUCUCUCUUCGCCACC 22

Db 25 ATTGCTTCGTTGCCACC 5

##### RESULT 2

US-10-719-900-980988

; Sequence 980988, Application US/10719900

; Publication No. US20050026164A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

; FILE REFERENCE: 3528.1

Query Match 66.7%; Score 16; DB 10; Length 25;  
Best Local Similarity 45.8%; Pred. No. 4.5e+03;  
Matches 11; Conservative 8; Mismatches 5; Indels

FILE REFERENCE: AM101083 (031896-042000)  
CURRENT APPLICATION NUMBER: US/11/060,756  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 47788  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe  
US-11-060-756-47788

Query Match 66.7%; Score 16; DB 13; Length 25;  
Best Local Similarity 45.8%; Pred. No. 4.5e+03;  
Matches 11; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 1 UAUGUCUCUCUCCUUGCCACCUC 24  
Db 25 TAATCTCCCTCCCTTCCACATC 2

## RESULT 8

US-10-310-914A-205339  
Sequence 205339, Application US/10310914A  
Publication No. US2005003322A1

## GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac  
APPLICANT: Shiller, Kvazat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310,914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 205339  
LENGTH: 24  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-205339

Query Match 65.8%; Score 15.8; DB 11; Length 24;  
Best Local Similarity 89.5%; Pred. No. 5.5e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AUGUCUCUCUCCUUGGCCA 20  
Db 5 AUGUCUCUCUCCUUGGCCA 23

## RESULT 9

US-11-136-527-276878  
Sequence 276878, Application US/11136527  
Publication No. US20050287570A1

## GENERAL INFORMATION:

APPLICANT: Wyeth  
APPLICANT: Mounts, William M  
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
FILE REFERENCE: 031896-041000 (AM101086)  
CURRENT APPLICATION NUMBER: US/11/136,527  
CURRENT FILING DATE: 2005-05-25  
PRIOR APPLICATION NUMBER: US 60/574,294  
PRIOR FILING DATE: 2005-05-26  
NUMBER OF SEQ ID NOS: 362830  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 276878  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Probe  
US-11-136-527-276878

Query Match 65.8%; Score 15.8; DB 16; Length 25;

Best Local Similarity 47.4%; Pred. No. 5.5e+03;  
Matches 9; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AUGUCUCUCUCCUUGGCCA 20  
Db 6 ATTGCTGCTCCTTTGGCCA 24

## RESULT 10

US-11-136-527-276903  
Sequence 276903, Application US/11136527  
Publication No. US20050287570A1

## GENERAL INFORMATION:

APPLICANT: Wyeth  
APPLICANT: Mounts, William M  
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
FILE REFERENCE: 031896-041000 (AM101086)  
CURRENT APPLICATION NUMBER: US/11/136,527  
CURRENT FILING DATE: 2005-05-25  
PRIOR APPLICATION NUMBER: US 60/574,294  
PRIOR FILING DATE: 2005-05-26  
NUMBER OF SEQ ID NOS: 362830  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 276903  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Probe  
US-11-136-527-276903

Query Match 65.8%; Score 15.8; DB 16; Length 25;  
Best Local Similarity 47.4%; Pred. No. 5.5e+03;  
Matches 9; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AUGUCUCUCUCCUUGGCCA 20  
Db 2 ATTGCTGCTCCTTTGGCCA 20

## RESULT 11

US-10-719-900-678730  
Sequence 678730, Application US/10719900  
Publication No. US20050026164A1

## GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou  
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
FILE REFERENCE: 3528.1  
CURRENT APPLICATION NUMBER: US/10/719,900  
CURRENT FILING DATE: 2003-11-20  
PRIOR APPLICATION NUMBER: 60/427,808  
PRIOR FILING DATE: 2002-11-20  
NUMBER OF SEQ ID NOS: 982914  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 678730  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-719-900-678730

Query Match 65.0%; Score 15.6; DB 9; Length 25;  
Best Local Similarity 45.5%; Pred. No. 6.7e+03;  
Matches 10; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 1 UAUGUCUCUCUCCUUGCCACC 22  
Db 2 TATTGCTCAGCTTTAGTCACC 23

## RESULT 12

US-11-036-317-35846  
Sequence 35846, Application US/11036317  
Publication No. US20050214823A1

```

US-10-956-157-21624

Query Match      64.2%; Score 15.4; DB 10; Length 25;
Best Local Similarity 47.1%; Pred. No. 8.2e+03;
Matches      8; Conservative      8; Mismatches      1; Indels      0; Gaps      0;

QY      2 AUUGUCUCUCUUUCGC 18
      ||::||::||::||
DB      23 ATTGCTCTCCTTTCTC 7

RESULT 15
US-10-956-157-21630/c
; Sequence 21630, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 21630
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-21630

Query Match      64.2%; Score 15.4; DB 10; Length 25;
Best Local Similarity 47.1%; Pred. No. 8.2e+03;
Matches      8; Conservative      8; Mismatches      1; Indels      0; Gaps      0;

QY      2 AUUGUCUCUCUUUCGC 18
      ||::||::||::||
DB      22 ATTGCTCTCCTTTCTC 6

Search completed: June 19, 2007, 16:27:50
Job time : 1264 secs

```

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 13:01:51 ; Search time 610 Seconds  
(without alignments)  
405.912 Million cell u

**Title:** US-10-604-726A-5136

Perfect score: 24  
Sequence: 1 uauuqucucuccuuuucqccaccuc 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 15754707 seqs, 5162687648 residues

Total number of hits satisfying chosen parameters: 17957554

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0\$

Maximum Match 100%

## Listing first 45 summaries

Database : Published Announcements NA New.\*

```

Database :
Published Applications NA, New:**
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08 NEW PUB.seq:
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06 NEW PUB.seq:
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07 NEW PUB.seq:
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT NEW PUB.seq:
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US05 NEW PUB.seq:
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10 NEW PUB.seq:
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10 NEW PUB.seq1:
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10 NEW PUB.seq2:
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10 NEW PUB.seq3:
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10 NEW PUB.seq4:
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10 NEW PUB.seq5
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10 NEW PUB.seq6
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11 NEW PUB.seq:
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11 NEW PUB.seq1
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11 NEW PUB.seq2
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11 NEW PUB.seq3
17: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11 NEW PUB.seq4
18: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11 NEW PUB.seq5
19: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11 NEW PUB.seq6
20: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11 NEW PUB.seq7
21: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10 NEW PUB.seq8
22: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10 NEW PUB.seq9

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	16	66.7	25	11	US-10-956-160-171431	Sequence 171431,
2	15	62.5	19	10	US-10-714-333A-661177	Sequence 661177,
3	15	62.5	19	17	US-11-093-832-661177	Sequence 661177,
			25	11	US-10-956-160-13205	Sequence 13205, A
C 5	15	62.5	25	11	US-10-956-160-25233	Sequence 25233, A
C 6	14.8	61.7	19	8	US-10-709-691B-2187318	Sequence 2187318,
C 7	14.8	61.7	19	8	US-10-709-691B-2187318	Sequence 2187318,
C 8	14.6	60.8	25	14	US-11-217-529-33285	Sequence 33285, A
C 9	14.4	60.0	19	10	US-10-714-333A-928822	Sequence 928822,
	10	14.4	60.0	19	US-10-714-333A-1077569	Sequence 1077569,
C 11	14.4	60.0	19	10	US-10-714-333A-1245669	Sequence 1245669,

US-10-7/14-333A-661177  
; Sequence 661177, Application US/10714333A  
; Publication No. US20070031844A1  
; GENERAL INFORMATION:

## ALIGNMENTS

```

RESULT 1
US-10-956-160-171431
; Sequence 171431, Application US
; Publication No. US2007000899A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC AC
; TITLE OF INVENTION: MODELS OF
; FILE REFERENCE: 031896-044000
; CURRENT APPLICATION NUMBER: US-
; CURRENT FILING DATE: 2004-10-
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 171431
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-171431

```

Query Match 66.7%; Score 16; DB 11; Length 25;  
Best Local Similarity 41.7%; Pred. No. 2.9e+03;  
Matches 10: Conservative 9; Mismatches 5; Indels 0;  
Caps 0;

**QY**

1 UAUGUCUCUCCUUUGCACCTC 24  
      : : -:|:-||::| ||:|

**DB**

1 TGPAGTCTCTCCTTTGACTACCTC 24

RESULT 2  
US-10-714-333A-661177  
; Sequence 661177, Application US/10714333A  
; Publication No. US2007003184A1  
; GENERAL INFORMATION:

```

; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333A
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 661177
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-714-333A-661177

Query Match 62.5%; Score 15; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UAUGUCUCUCCUUU 15
Db 5 UAUGUCUCUCCUUU 19

RESULT 3
US-11-093-832-661177
; Sequence 661177, Application US/11093832
; Publication No. US20070039072A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/093,832
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 661177
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-093-832-661177

Query Match 62.5%; Score 15; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UAUGUCUCUCCUUU 15
Db 5 UAUGUCUCUCCUUU 19

RESULT 4
US-10-956-160-13205
; Sequence 13205, Application US/10956160
; Publication No. US20070009899A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13205
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
; US-10-956-160-13205

Query Match 62.5%; Score 15; DB 11; Length 25;
Best Local Similarity 47.8%; Pred. No. 8.2e+03;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AUUGUCUCUCCUUUGCCACCUC 24
Db 1 ATTGGCTCTGAATTAGCACCTC 23

RESULT 5
US-10-956-160-25233/c
; Sequence 25233, Application US/10956160
; Publication No. US20070009899A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25233
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
; US-10-956-160-25233

Query Match 62.5%; Score 15; DB 11; Length 25;
Best Local Similarity 43.5%; Pred. No. 8.2e+03;
Matches 10; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 1 UAUGUCUCUCCUUUGCCACCUC 23
Db 23 TCTGGTCTCTCTCTGGCTCTCT 1

RESULT 6
US-10-709-691B-2175725/c
; Sequence 2175725, Application US/10709691B
; Publication No. US20070031843A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Avniel, Amir
; TITLE OF INVENTION: Bioinformatically Detectable Group of Novel Regulatory Bacterial
; FILE REFERENCE: EIS23
; CURRENT APPLICATION NUMBER: US/10/709,691B
; CURRENT FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 4254815
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2175725
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Streptococcus pneumoniae R6

```

## US-10-709-691B-2175725

Query Match 61.7%; Score 14.8; DB 8; Length 19;  
Best Local Similarity 38.9%; Pred. No. 9.8e+03;  
Matches 7; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

Qy 1 UAUGUCUCUCCUUCGC 18  
Db 19 TATTTTCTCCTTCGC 2

## RESULT 7

US-10-709-691B-2187318/c  
; Sequence 2187318, Application US/10709691B  
; Publication No. US20070031843A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; APPLICANT: Bentwich, Itzhak  
; APPLICANT: Avniel, Amir  
; TITLE OF INVENTION: Bioinformatically Detectable Group of Novel Regulatory Bacterial  
; TITLE OF INVENTION: and Bacterial Associated Oligonucleotides and Uses Thereof  
; FILE REFERENCE: Efs23  
; CURRENT APPLICATION NUMBER: US/10/709,691B  
; CURRENT FILING DATE: 2004-05-24  
; NUMBER OF SEQ ID NOS: 4254815  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2187318  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Streptococcus pneumoniae R6

## US-10-709-691B-2187318

Query Match 61.7%; Score 14.8; DB 8; Length 19;  
Best Local Similarity 38.9%; Pred. No. 9.8e+03;  
Matches 7; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

Qy 1 UAUGUCUCUCCUUCGC 18  
Db 18 TATTTTCTCCTTCGC 1

## RESULT 8

US-11-217-529-33285  
; Sequence 33285, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHIISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 33285  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus

## US-11-217-529-33285

Query Match 60.8%; Score 14.6; DB 14; Length 25;  
Best Local Similarity 42.9%; Pred. No. 1.2e+04;  
Matches 9; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 3 UUGUCUCUCCUUCGCCACCU 23  
Db 4 TTGCTCTTCATTGGACACCT 24

## RESULT 9

US-10-714-333A-928822/c  
; Sequence 928822, Application US/10714333A  
; Publication No. US20070031844A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/10/714,333A  
; CURRENT FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 928822  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens

## US-10-714-333A-928822

Query Match 60.0%; Score 14.4; DB 10; Length 19;  
Best Local Similarity 37.5%; Pred. No. 1.5e+04;  
Matches 6; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

Qy 1 UAUGUCUCUCCUUC 16  
Db 16 TATGTTTCTCCTTC 1

## RESULT 10

US-10-714-333A-1077569  
; Sequence 1077569, Application US/10714333A  
; Publication No. US20070031844A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/10/714,333A  
; CURRENT FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1077569  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens

## US-10-714-333A-1077569

Query Match 60.0%; Score 14.4; DB 10; Length 19;  
Best Local Similarity 93.8%; Pred. No. 1.5e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 UAUGUCUCUCCUUC 16  
Db 3 UAUGUCUCUCCUUC 18



RESULT 11  
 US-10-714-333A-1245669/c  
 ; Sequence 1245669, Application US/10714333A  
 ; Publication No. US20070031844A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmakon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/10/714,333A  
 ; CURRENT FILING DATE: 2003-11-14  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 1245669  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-10-714-333A-1245669

Query Match 60.0%; Score 14.4; DB 10; Length 19;  
 Best Local Similarity 37.5%; Pred. No. 1.5e+04;  
 Matches 6; Conservative 9; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 UAUGUCUCUCCUUC 16  
 :|:::|:|:|:|:|:|  
 Db 16 TATTCTCTCTCTTC 1

RESULT 12  
 US-10-714-333A-1245759/c  
 ; Sequence 1245759, Application US/10714333A  
 ; Publication No. US20070031844A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmakon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/10/714,333A  
 ; CURRENT FILING DATE: 2003-11-14  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 1245759  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-10-714-333A-1245759

Query Match 60.0%; Score 14.4; DB 10; Length 19;  
 Best Local Similarity 37.5%; Pred. No. 1.5e+04;  
 Matches 6; Conservative 9; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 UAUGUCUCUCCUUC 16  
 :|:::|:|:|:|:|:|  
 Db 18 TATTCTCTCTCTTC 3

RESULT 13  
 US-11-093-832-928822/c  
 ; Sequence 928822, Application US/11093832  
 ; Publication No. US20070039072A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmakon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/093,832  
 ; CURRENT FILING DATE: 2005-03-29  
 ; PRIOR APPLICATION NUMBER: US/10/714,333  
 ; PRIOR FILING DATE: 2003-11-14  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 928822  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-093-832-928822

Query Match 60.0%; Score 14.4; DB 17; Length 19;  
 Best Local Similarity 37.5%; Pred. No. 1.5e+04;  
 Matches 6; Conservative 9; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 UAUGUCUCUCCUUC 16  
 :|:::|:|:|:|:|:|  
 Db 16 TATTGTTCTCTTC 1

RESULT 14  
 US-11-093-832-1077569  
 ; Sequence 1077569, Application US/11093832  
 ; Publication No. US20070039072A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmakon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/093,832  
 ; CURRENT FILING DATE: 2005-03-29  
 ; PRIOR APPLICATION NUMBER: US/10/714,333  
 ; PRIOR FILING DATE: 2003-11-14  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 1077569  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-093-832-1077569

Query Match 60.0%; Score 14.4; DB 17; Length 19;  
 Best Local Similarity 93.8%; Pred. No. 1.5e+04;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 UAUGUCUCUCCUUC 16  
 |||||:|:|:|:|:|:|

Db 3 UAUGUCUCUCCUUC 18

RESULT 15

US-11-093-832-1245669/c  
 ; Sequence 1245669, Application US/11093832  
 ; Publication No. US20070039072A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/093,832  
 ; CURRENT FILING DATE: 2005-03-29  
 ; PRIOR APPLICATION NUMBER: US/10/714,333  
 ; PRIOR FILING DATE: 2003-11-14  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 1245669  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-093-832-1245669

Query Match 60.0%; Score 14.4; DB 17; Length 19;  
 Best Local Similarity 37.5%; Pred. No. 1.5e+04;  
 Matches 6; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY 1 UAUGUCUCUCCUUC 16  
 :|:::|::|::|  
 Db 16 TATTCCTCTCTTC 1

Search completed: June 19, 2007, 13:30:35  
 Job time : 611.5 secs

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 12:49:12 ; Search time 6876 Seconds  
(without alignments)  
216.548 Million cell updates/sec

Title: US-10-604-726A-5136

Perfect score: 24  
Sequence: 1 uaugucucuccuucgaccacc 24

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 35954

Minimum DB seq length: 0  
Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*\*  
1: gb\_est1:\*\*  
2: gb\_est3:\*\*  
3: gb\_est4:\*\*  
4: gb\_est5:\*\*  
5: gb\_est6:\*\*  
6: gb\_est7:\*\*  
7: gb\_est8:\*\*  
8: gb\_est9:\*\*  
9: gb\_est10:\*\*  
10: gb\_est11:\*\*  
11: gb\_est12:\*\*  
12: gb\_est13:\*\*  
13: gb\_est14:\*\*  
14: gb\_est15:\*\*  
15: gb\_est16:\*\*  
16: gb\_est17:\*\*  
17: gb\_est18:\*\*  
18: gb\_est19:\*\*  
19: gb\_est20:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	13.4	55.8	25	15	AZ775852 2M0009N01
C 2	12.2	50.8	24	5	CA850924 D08B11 D2
C 3	12	50.0	23	15	AZ329650 1M0054A13
C 4	12	50.0	23	15	AZ514958 1M0054A13
C 5	11.6	48.3	21	15	AZ475883 1M0294J14
C 6	11.6	48.3	25	1	A1539240 tp64b08.x
C 7	11.2	46.7	18	9	CN750241 ApdT-VIII
C 8	11.2	46.7	21	19	AG189071 Pan trogl
C 9	11.2	46.7	21	19	AG202804 Pan trogl
C 10	11.2	46.7	22	10	CO788412 NT004AG0
C 11	11.2	46.7	25	17	CL692271 PRI0158C
C 12	11	45.8	19	17	CL671134 PRI0163D
C 13	11	45.8	22	1	AU014100
C 14	11	45.8	22	1	AU014106 AU014106

15	11	45.8	22	15	AZ942905
16	11	45.8	23	19	CT014183
C 17	10.8	45.0	25	1	A1527253
18	10.8	45.0	25	15	AZ479489
19	10.6	44.2	19	15	AZ345425
C 20	10.6	44.2	22	19	TA376G03Q
C 21	10.6	44.2	23	1	AJ797058
22	10.6	44.2	23	13	DN759071
23	10.6	44.2	23	15	AZ499076
24	10.6	44.2	23	18	DX598444
25	10.6	44.2	24	1	AJ792029
26	10.6	44.2	24	19	AJ601047
27	10.6	44.2	25	2	BG925523
28	10.6	44.2	25	11	Z20702
29	10.6	44.2	25	15	AZ333213
C 30	10.6	44.2	25	15	AZ346715
C 31	10.6	44.2	25	15	AZ490095
C 32	10.4	43.3	21	8	CD533377
C 33	10.4	43.3	21	8	CF318419
C 34	10.4	43.3	21	13	DN955270
C 35	10.4	43.3	22	1	AU014275
C 36	10.4	43.3	23	15	AZ658085
C 37	10.4	43.3	24	16	BH790181
C 38	10.2	42.5	15	18	DX597598
C 39	10.2	42.5	18	2	BG900971
C 40	10.2	42.5	18	19	AJ587746
C 41	10.2	42.5	19	15	AZ854740
C 42	10.2	42.5	20	19	AG202286
C 43	10.2	42.5	21	15	AZ342500
C 44	10.2	42.5	21	15	AZ342500
C 45	10.2	42.5	22	1	A1057600

## ALIGNMENTS

RESULT 1  
LOCUS AZ775852/c 25 bp DNA linear GSS 16-FEB-2001  
DEFINITION 2M0009N01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0009N01 F, genomic survey sequence.  
ACCESSION AZ775852  
VERSION AZ775852.1 GI:12902821  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Seq primer: CGTTGTAACGACGCCAGT  
Class: Plasmid ends  
High quality sequence stop: 25.  
Location/Qualifiers  
1. .25  
/organism="Mus musculus"



with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 50.0%; Score 12; DB 15; Length 23;  
Best Local Similarity 50.0%; Pred. No. 1.5e+06;  
Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAUGUCUCUCC 12  
:|:|:|:|:|:|  
Db 11 TATTGTCCTCC 22

## RESULT 4

AZ514958 23 bp DNA linear GSS 05-OCT-2000  
LOCUS  
DEFINITION IM0054A13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0054A13 F, genomic survey sequence.

ACCESSION AZ514958

VERSION AZ514958.1 GI:10696274

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.

## REFERENCE

## AUTHORS

1 (bases 1 to 23)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

## COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0054 row: A column: 13

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 23.

## FEATURES

## source

1..23

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0054A13"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 50.0%; Score 12; DB 15; Length 23;  
Best Local Similarity 50.0%; Pred. No. 1.5e+06;  
Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAUGUCUCUCC 12  
:|:|:|:|:|:|  
Db 11 TATTGTCCTCC 22

## RESULT 5

## LOCUS

DEFINITION IM0294J14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0294J14 F, genomic survey sequence.

ACCESSION AZ475883

VERSION AZ475883.1 GI:10634008

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.

## REFERENCE

## AUTHORS

1 (bases 1 to 21)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

## COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0294 row: J column: 14

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

## FEATURES

## source

1..21

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0294J14"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 48.3%; Score 11.6; DB 15; Length 21;  
Best Local Similarity 44.4%; Pred. No. 2.2e+06;  
Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 7 CUCUCCUUGGCCACCU 24

Db 21 CTCCTCTCTCCCTTC 4

## RESULT 6

AI539240/c  
LOCUS  
DEFINITION  
tp64b08.x1 NCI CGAP Ut3 Homo sapiens cDNA clone IMAGE:2204055 3'  
similar to TR:Q40726 Q40726 DNA BINDING PROTEIN ; mRNA sequence.

ACCESSION  
AI539240

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 25)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: [cgaabs-r@mail.nih.gov](mailto:cgaabs-r@mail.nih.gov)

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality

Insert Length: 1192 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1

POLYA=No.

## FEATURES

source

Location/Qualifiers

1..25

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2204055"

/tissue\_type="poorly-differentiated endometrial

adenocarcinoma, 2 pooled tumors"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP Ut3"

/notes="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.45 kb. Life Technologies catalog #:

11541-018"

## ORIGIN

Query Match 48.3%; Score 11.6; DB 1; Length 25;

Best Local Similarity 44.4%; Pred. No. 2.3e+06;

Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 6 UCUCUCCUUGGCCACCU 23

Db 25 TTCCCTCTTCCCTCTCT 8

## RESULT 7

LOCUS

DEFINITION

ApDT-VIII-C12 ApDT Acyrthosiphon pisum cDNA clone ApDVIIC12 5',

linear mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Acyrthosiphon pisum (pea aphid)

Acyrthosiphon pisum

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;

Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 18)

REFERENCE

AUTHORS

Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,

Stern, D., Tagu, D. and Wincker, P.

An expressed sequence tags database for the pea aphid Acyrthosiphon

pisum

Unpublished (2004)

COMMENT

Contact: D. Tagu

INRA Rennes

UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France

Tel: +33-2-23-48-51-65

Fax: +33-2-23-48-51-50

Risk of contamination by bacterial sequences from obligatory

(Buchnera) or facultative endosymbionts.

PCR Primers

FORWARD: GCCGCATAACTTCGTATAGCA

Plate: VIII row: C column: 12.

Location/Qualifiers

1..18

/organism="Acyrthosiphon pisum"

/mol\_type="mRNA"

/cultivar="intra-lyon-bf21 1101"

/db\_xref="taxon:7029"

/clone="ApDVIIC12"

/tissue\_type="digestive track"

/dev\_stage="adults, parthenogenetic females"

/lab\_host="ApDT"

/note="Vector: pDNR-LIB; Site 1: SfiIA; Site 2: SfiIB;

Sample name: ApDT; plant growth place: UMR INRA-INGA BP21

; Sowing date: 03/04/2003; Harvesting date: 12/06/2003;

Description: Long photoperiod 16-hr light/8-hr dark at 20

C; no overcrowding; grown on Vicia faba 3-wk old seedlings

sown under non sterile condition; experimental

condition: standard, see description"

## ORIGIN

Query Match 46.7%; Score 11.2; DB 9; Length 18;

Best Local Similarity 31.2%; Pred. No. 3.3e+06;

Matches 5; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 UAUUGUCUCCUUC 16

Db 16 TCTTTCTCTCTCTC 1

## RESULT 8

LOCUS

DEFINITION

Pan troglodytes DNA, clone: RP43-063G02.T7, genomic survey

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Pan troglodytes (chimpanzee)

Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
LIBRARY
Sequencing: T7
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
Location/Qualifiers
1. .21
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-086J05.T7"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"
ORIGIN
Query Match 46.7%; Score 11.2; DB 19; Length 21;
Best Local Similarity 56.2%; Pred. No. 3.3e+06;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 7 CUCUCUUUGGCCACC 22
| | | | | | | |
6 CCTCTCTTCCCCCCC 21
RESULT 10
CO788412 linear EST 05-AUG-2004
LOCUS NT004A.G01 St18-22 Neural tube (NT) Ambystoma mexicanum cDNA 5',
DEFINITION similar to hypothetical protein, mRNA sequence.
ACCESSION CO788412
VERSION CO788412.1 GI:51004383
KEYWORDS EST.
SOURCE Ambystoma mexicanum (axolotl)
ORGANISM Ambystoma mexicanum
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
Ambystoma.
1 (bases 1 to 22)
Habermann,B., Bebin,A.G., Herklotz,S., Volkmer,M., Eckelt,K.,
Pehlke,K., Epperlein,H.H., Schackert,H.K., Wiebe,G. and Tanaka,B.M.,
An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
expressed sequence tags from embryonic and regenerating blastema
cDNA libraries
Genome Biol. 5 (9), R67 (2004)
15345051
Contact: Elly M. Tanaka
Tanaka Lab
Max Planck Institute of Molecular Cell Biology and Genetics,
Dresden
Pfotenhauserstrasse 108, 01307 Dresden, Germany
Tel: 0049 351 210 2620
Fax: 0049 351 210 1489
Email: tanaka@mpi-cbg.de
Plate: NT004A row: 01 column: G
Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
Location/Qualifiers
1. .22
/organism="Ambystoma mexicanum"
/mol_type="mRNA"
/db_xref="taxon:8296"
/tissue_type="Neural Tube, Notochord, Somites"
/cell_type="Includes Neural tube, notochord, somites"
/dev_stages="Stage 18-22"
/clone_lib="St18-22 Neural tube (NT)"
/note="Vector: pCMVSPORT6; Site_1: NotI; Site_2: SalI;
Unnormalized cDNA plasmid library prepared by Invitrogen.
Size fractionated mRNA was polydt primed and cloned into
NotI-SalI site of pCMVSPORT6. Bacterial host is
EMDH108-TONA. Average insert size is 1.5 kb."
FEATURES
source

```





into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, <http://www.nirs.go.jp>)"

## ORIGIN

Query Match 45.8%; Score 11; DB 1; Length 22;  
Best Local Similarity 30.0%; Pred. No. 4.1e+06;  
Matches 6; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 4 UGUCUCUCCUUGCCACCU 23

Db 3 TGTATGTCCTTCAACACT 22

## RESULT 14

AU014106

LOCUS

DEFINITION AU014106 Schizosaccharomyces pombe late log phase cDNA

Accession AU014106 Schizosaccharomyces pombe cDNA clone spc09175, mRNA sequence.

Version AU014106

Keywords EST.

Source AU014106.1 GI:3368897

Organism Schizosaccharomyces pombe (fission yeast)

Organism Schizosaccharomyces pombe

Reference Rukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

Authors Schizosaccharomycetales; Schizosaccharomycetaceae;

Title Schizosaccharomycetes.

1 (bases 1 to 22)

Moriyomo, M. and Mita, K.

Identification of expressed sequence tags of Schizosaccharomycetes

pombe

Journal Unpublished (1998)

Contact: Mitsuoki Moriyomo

Genome Research Group

National Institute of Radiological Sciences

9-1, Anagawa-4-chome, Inage-Ku, Chiba, Chiba 263-8555, Japan

Email: moriyomo@nirs.go.jp.

Location/Qualifiers

1..22

Organism="Schizosaccharomyces pombe"

Mol\_type="mRNA"

Strain="972"

DB\_xref="taxon:4896"

Clone="spc09175"

Sex="h minus"

Clone\_lib="Schizosaccharomyces pombe late log phase cDNA"

Notes="Vector: M13mp19; The cDNA library of

Schizosaccharomyces pombe was prepared by cloning cDNA

into the SmaI site of M13mp19 DNA and the direction of

sequences was not always from 5' to 3'. The cDNA data of

Schizosaccharomyces pombe are available for searching on

the World Wide Web. (URL, <http://www.nirs.go.jp>)"

ORIGIN

Query Match 45.8%; Score 11; DB 1; Length 22;  
Best Local Similarity 30.0%; Pred. No. 4.1e+06;  
Matches 6; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 4 UGUCUCUCCUUGCCACCU 23

Db 3 TGTATGTCCTTCAACACT 22

## RESULT 15

AZ942905

LOCUS

DEFINITION AZ942905 22 bp DNA linear GSS 26-APR-2001

Accession AZ942905 2M0203K13F Mouse 10kb plasmid UUGC2M library Mus musculus genomic

Version AZ942905.1 GI:13806556

Keywords GSS..

Source Mus musculus (house mouse)

## ORGANISM

Mus musculus

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 22)

Authors

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhauser, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)

Insert Length: 10000 Std Error: 0.00

Plate: 0203 row: K column: 13

Seq primer: CGTGTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22

Organism="Mus musculus"

Mol\_type="genomic DNA"

Strain="C57BL/6J"

DB\_xref="taxon:10090"

Clone="UUGC2M0203K13"

Sex="Female"

Lab host="E. coli strain XL10-Gold, TI-resistant, P-"

Clone\_lib="Mouse 10kb plasmid UUGC2M library"

Note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 [gi|4732114|gb|AF129072.1], a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

ORIGIN

Query Match 45.8%; Score 11; DB 15; Length 22;  
Best Local Similarity 42.1%; Pred. No. 4.1e+06;  
Matches 8; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 6 UCUCUCUCCUUGCCACCU 24

Db 2 TCCTTCTCTCTCTCTCTC 20

Search completed: June 19, 2007, 20:24:46  
Job time : 6879 secs

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 15:44:15 ; Search time 10160 Seconds  
(without alignments)  
578.270 Million cell updates/sec

Title: US-10-604-726A-6033  
Perfect score: 85  
Sequence: 1 ggguaucugcacacagag.....uuuucuggagcagaguccu 85

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 3800530

Minimum DB seq length: 0  
Maximum DB seq length: 85

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
1: gb\_env:\*  
2: gb\_pat:\*  
3: gb\_ph:\*  
4: gb\_pl:\*  
5: gb\_pr:\*  
6: gb\_ro:\*  
7: gb\_sts:\*  
8: gb\_sy:\*  
9: gb\_un:\*  
10: gb\_vic:\*  
11: gb\_ov:\*  
12: gb\_htg:\*  
13: gb\_in:\*  
14: gb\_om:\*  
15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21.4	25.2	50	2 AR683427	AR683427 Sequence
2	21.4	25.2	50	2 AR824195	AR824195 Sequence
C 3	20.8	24.5	76	2 BD437654	BD437654 POLYNUCLE
C 4	20.8	24.5	76	2 AX455957	AX455957 Sequence
C 5	20.8	24.5	76	10 AY047230S1	AY047230 HIV-1 TVO
6	20	23.5	60	2 BD469930	BD469930 OLIGONUCL
7	20	23.5	60	2 CQ539417	CQ539417 Sequence
8	19.8	23.3	83	2 AX982586	AX982586 Sequence
9	19.8	23.3	83	2 BD117445	BD117445 EST and e
10	19.8	23.3	83	2 AR421892	AR421892 Sequence
11	19.2	22.6	51	2 DD162947	DD162947 Nucleic A
C 12	19.2	22.6	65	5 AF011577	AF011577 Homo sapi
C 13	19.2	22.6	65	2 BD487569	BD487569 OLIGONUCL
14	19.2	22.6	65	2 CQ557056	CQ557056 Sequence
15	19	22.4	50	2 AR86075	AR86075 Sequence
16	19	22.4	50	2 AR826843	AR826843 Sequence
C 17	19	22.4	51	5 HSDTCRV03	227181 H. sapiens r
18	18.8	22.1	50	2 CQ005106	CQ005106 Sequence

19	18.8	22.1	50	2 CQ005107	CQ005107 Sequence
20	18.8	22.1	60	5 S49071	S49071 immunoglob
C 21	18.8	22.1	61	2 BD225196	BD225196 Human pap
C 22	18.8	22.1	61	2 CS195912	CS195912 Sequence
23	18.8	22.1	65	2 BD464903	BD464903 OLIGONUCL
24	18.8	22.1	65	2 CQ534390	CQ534390 Sequence
25	18.8	22.1	83	5 HUMSPRC40	M61813 Human alpha
26	18.6	21.9	51	2 AX159481	AX159481 Sequence
27	18.6	21.9	60	2 BD467993	BD467993 OLIGONUCL
28	18.6	21.9	60	2 CQ537480	CQ537480 Sequence
C 29	18.6	21.9	65	2 BD460907	BD460907 OLIGONUCL
C 30	18.6	21.9	65	2 CQ530394	CQ530394 Sequence
C 31	18.6	21.9	68	2 AS9167	AS9167 Sequence 59
C 32	18.6	21.9	68	2 AR073648	AR073648 Sequence
C 33	18.6	21.9	76	2 AS9169	AS9169 Sequence 61
C 34	18.6	21.9	76	2 AS9170	AS9170 Sequence 62
C 35	18.6	21.9	76	2 AS9173	AS9173 Sequence 65
C 36	18.6	21.9	76	2 AS9174	AS9174 Sequence 66
C 37	18.6	21.9	76	2 AR073650	AR073650 Sequence
38	18.6	21.9	76	2 AR073651	AR073651 Sequence
C 39	18.6	21.9	76	2 AR073654	AR073654 Sequence
40	18.6	21.9	76	2 AR073655	AR073655 Sequence
41	18.4	21.6	43	2 AR104022	AR104022 Sequence
42	18.4	21.6	43	2 AR104055	AR104055 Sequence
C 43	18.4	21.6	43	2 AR104056	AR104056 Sequence
C 44	18.4	21.6	43	2 AR104057	AR104057 Sequence
45	18.4	21.6	69	2 AR61027	AR61027 Sequence 33

ALIGNMENTS

RESULT 1  
LOCUS AR683427 50 bp DNA linear PAT 12-SEP-2005  
DEFINITION Sequence 2856 from patent US 6905827.  
ACCESSION AR683427  
VERSION AR683427.1 GI:74465197  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Wohlgemuth,J., Fry,K., Woodward,R. and Ly,N.  
TITLE Methods and compositions for diagnosing or monitoring auto immune and chronic inflammatory diseases  
JOURNAL Patent: US 6905827-A 2856 14-JUN-2005;  
FEATURES Expression Diagnostics, Inc.; So. San Francisco, CA  
Location/Qualifiers  
source 1..50  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match	25.2%;	Score 21.4;	DB 2;	Length 50;
Best Local Similarity	41.0%;	Pred. No. 1.3e+04;		
Matches	16;	Conservative 12;	Mismatches 11;	Indels 0;
Gaps	0;			
Qy	42	AGUUGAAGGCGGCUUCUCUGUUUUGGAGCAGA 80		
Db	1	AGTCCCAAGGTGTTTGTCTACTGTTTCTCCATGAATA 39		
RESULT 2				
AR824195				
LOCUS AR824195 50 bp DNA linear PAT 10-AUG-2006				
DEFINITION Sequence 2856 from patent US 7026121.				
ACCESSION AR824195				
VERSION AR824195.1 GI:111848010				
KEYWORDS				
SOURCE Unknown.				
ORGANISM Unknown.				
Unclassified.				

SOURCE	synthetic construct synthetic construct other sequences; artificial sequences.
ORGANISM	1
REFERENCE	zur Megede,J., Barnett,S.W., Engelbrecht,S. and van Rensburg,E. Polynucleotides encoding antigenic hiv type c polypeptides, polypeptides and uses thereof
AUTHORS	Patent: WO 0204493-A 73 17-JAN-2002;
TITLE	CHIRON CORPORATION (US); University of Stellenbosch (ZA)
JOURNAL	Location/Qualifiers
FEATURES	1..76 /organism=synthetic construct" /mol_type=unassigned DNA" /db_xref=taxon:32630" /note="HIV Type C RevExon1 Wild Type"
source	
ORIGIN	
Query Match	24.5%; Score 20.8; DB 2; Length 76; Best Local Similarity 41.1%; Pred. No. 2.2e+04; Matches 23; Conservative 11; Mismatches 22; Indels 0; Gaps 0;
QY	15 UGAGAGGGCGUGUUAAGGCCGUCCCAAGUGAAGGCUGCUCUUUGCUUGUUUC 70       :   :   :   :       :   :   :   71 TGTATAGAGGATTTTGATGATCTTCACCACTTGGAGGAGCGCTTCGTCGTCTCC 16
Db	
RESULT 5	
AY047230S1/c	76 bp DNA linear VRL 22-FEB-2002
LOCUS	AY047230S1
DEFINITION	HIV-1 TV001 from South Africa Rev (rev) gene, exon 1.
ACCSSION	AY047230
VERSION	AY047230.1 GI:16554987
KEYWORDS	1 of 2
SEGMENT	Human immunodeficiency virus 1 (HIV-1)
SOURCE	Human immunodeficiency virus 1
ORGANISM	Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae; Lentivirus; Primate lentivirus group. 1 (bases 1 to 76) Scriba,T.J., de Villiers,T., Treurnicht,F.K., zur Megede,J., Barnett,S.W., Engelbrecht,S. and van Rensburg,E.J. Characterization of the South African HIV type 1 subtype C complete 5' long terminal repeat, nef, and regulatory genes AIDS Res. Hum. Retroviruses 18 (2), 149-159 (2002)
REFERENCE	11839148 2 (bases 1 to 76) Scriba,T.J., de Villiers,T., Treurnicht,F.K., zur Megede,J., Barnett,S.J., Engelbrecht,S. and Janse van Rensburg,E. Direct Submission Submitted (04-JUL-2001) Department of Medical Virology, University of Stellenbosch, PO Box 19063, Tygerberg, Western Cape 7505, South Africa
AUTHORS	
TITLE	
JOURNAL	
PUBMED	
FEATURES	Location/Qualifiers 1..76 /organism=Human immunodeficiency virus 1" /proviral /mol_type="genomic DNA" /isolate="TV001" /db_xref=taxon:11676" /country="South Africa" /note="Subtype: C" 1..76 /gene="rev" /number=1
source	
exon	
ORIGIN	
Query Match	24.5%; Score 20.8; DB 10; Length 76; Best Local Similarity 41.1%; Pred. No. 2.2e+04; Matches 23; Conservative 11; Mismatches 22; Indels 0; Gaps 0;
QY	15 UGAGAGGGCGUGUUAAGGCCGUCCCAAGUGAAGGCUGCUCUUUGCUUGUUUC 70       :   :   :   :       :   :   :   71 TGTATAGAGGATTTTGATGATCTTCACCACTTGGAGGAGCGCTTCGTCGTCTCC 16
Db	

Query Match	23.5%;	Score 20;	DB 2;	Length 60;
Best Local Similarity	38.9%;	Pred. No.	4.5e+04;	

FH	Key	Location/Qualifiers	
FT	source	1..83	
		/organism="Homo sapiens"	
FEATURES	Location/Qualifiers		
source	1..83		
	/organism="Homo sapiens"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:9606"		
ORIGIN			
Query Match	23.3%; Score 19.8; DB 2;	Length 83;	
Best Local Similarity	43.7%; Pred. No. 5.3e+04;		
Matches	31; Conservative 8; Mismatches 32; Indels 0; Gaps 0;		
QY	2 GGUAUCUGCAACUGAGAGGGCGGCUUAAAGCGGUCCCAAGUUUGAAGGCGGCUUUGCU 61		
Db	6 GGGCACCCTGCCTAGAGGTAGGTGGAACTCCATCCCCCATGAGCAGCGGCTCATCTCT 65		
QY	62 UCUGUUUUCUG 72		
Db	66 GCTGGTTCCCG 76		
RESULT 10			
AR421892			
LOCUS	AR421892	83 bp	DNA linear PAT 18-DEC-2003
DEFINITION	Sequence 13389 from patent US 6639063.		
ACCESSION	AR421892		
VERSION	AR421892.1 GI:40177002		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 83)		
AUTHORS	Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.		
TITLE	EST's and encoded human proteins		
JOURNAL	Patent: US 6639063-A 13389 28-OCT-2003;		
	Genset S.A.;;		
WGX;			
FEATURES	Location/Qualifiers		
source	1..83		
	/organism="unknown"		
	/mol_type="genomic DNA"		
ORIGIN			
Query Match	23.3%; Score 19.8; DB 2;	Length 83;	
Best Local Similarity	43.7%; Pred. No. 5.3e+04;		
Matches	31; Conservative 8; Mismatches 32; Indels 0; Gaps 0;		
QY	2 GGUAUCUGCAACUGAGAGGGCGGCUUAAAGCGGUCCCAAGUUUGAAGGCGGCUUUGCU 61		
Db	6 GGGCACCCTGCCTAGAGGTAGGTGGAACTCCATCCCCCATGAGCAGCGGCTCATCTCT 65		
QY	62 UCUGUUUUCUG 72		
Db	66 GCTGGTTCCCG 76		
RESULT 11			
DD162947			
LOCUS	DD162947	51 bp	DNA linear PAT 23-NOV-2005
DEFINITION	Nucleic Acids and Encoded Polypeptides Associated with Bipolar Disorder.		
ACCESSION	DD162947		
VERSION	DD162947.1 GI:83974597		
KEYWORDS	JP 2005508618-A/41.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;			
Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 51)		
AUTHORS	Evans,G.B		

```

FEATURES             Location/Qualifiers
     source
     1..65
     /organism="Mus musculus"
     /mol_type="unassigned DNA"
     /db_xref="taxon:10090"

ORIGIN

Query Match      22.6%; Score 19.2; DB 2; Length 65;
Best Local Similarity 41.7%; Pred. NO. 9.2e+04;
Matches 20; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY  25 UGUUAAGCGUCCCAAGUGAAGGCGCUUGUCUUGUUUUUG 72
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Dd  12 TGTGTAGTGGATCCCTGTGGAAGGCGCCATGCTTCTGCTCTG 59

RESULT 15
AR686075
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
     source
     1..50
     /organism="unknown"
     /mol_type="genomic DNA"

ORIGIN

Query Match      22.4%; Score 19; DB 2; Length 50;
Best Local Similarity 41.9%; Pred. NO. 1.1e+05;
Matches 18; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY  38 CCCAAGUUGAAGGCGCUUGUCUUGUUUUUGAUGCAGA 80
    ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Dd  2  CCTCAGTACAAGGGGCTTTGGAAGTGTTTGTGGCTGAATA 44

Search completed: June 19, 2007, 18:35:09
Job time : 10162 secs

```

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.  
OM nucleic - nucleic search, using sw model  
Run on: June 19, 2007, 15:35:52 ; Search time 314 Seconds  
(without alignments)  
2006.045 Million cell updates/sec

Title: US-10-604-726A-6033  
Perfect score: 85  
Sequence: 1 ggguaucgcaacagagag.....uuuucggaugcagaguccu 85  
Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0  
Searched: 5620219 seqs, 3705283702 residues  
Total number of hits satisfying chosen parameters: 6044068  
Minimum DB seq length: 0  
Maximum DB seq length: 85  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_200701.\*  
1: Geneseq1980s.\*  
2: Geneseq1990s.\*  
3: Geneseq2000s.\*  
4: Geneseq2001as.\*  
5: Geneseq2001bs.\*  
6: Geneseq2002as.\*  
7: Geneseq2002bs.\*  
8: Geneseq2003as.\*  
9: Geneseq2003bs.\*  
10: Geneseq2003cs.\*  
11: Geneseq2003ds.\*  
12: Geneseq2004as.\*  
13: Geneseq2004bs.\*  
14: Geneseq2005s.\*  
15: Geneseq2006s.\*  
16: Geneseq2007s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21.4	25.2	50	6 ABZ02865	Abz02865 Human leu
2	20.8	24.5	76	6 ABL33994	ABL33994 Wild type
3	20.8	24.5	76	12 ADM73807	Adm73807 HIV-1 pol
4	20	23.5	60	6 ABN36304	Abn36304 Human spl
5	19.6	23.1	51	10 ADK19849	Adk19849 Human man
6	19.6	23.1	74	10 ADK19487	Adk19487 Type IIS
7	19.2	22.6	60	15 ABK61465	Abk61465 Secreted
8	19.2	22.6	65	6 ABM53943	Abm53943 Mouse spl
9	19.2	22.6	80	12 ADM95921	Adm95921 Rat antis
10	19	22.4	50	6 ABZ05513	Abz05513 Human leu
11	19	22.4	60	14 AEC75978	Aec75978 Cancer pr
12	19	22.4	60	15 AEJ81361	Aej81361 Human cDN
13	18.8	22.1	50	4 AAL30539	Aal30539 Human SNP
14	18.8	22.1	50	4 AAL30538	Aal30538 Human SNP
15	18.8	22.1	60	2 RAX33875	Rax33875 HPV-16 in
16	18.8	22.1	65	6 ABN31277	Abn31277 Rat splic
17	18.8	22.1	70	14 ADZ27768	Adz27768 Chemosens

18	18.6	21.9	51	4 AAI75868	Aai75868 Human sil
19	18.6	21.9	60	6 ABN34367	Abn34367 Human spl
20	18.6	21.9	60	15 AEL67275	Ael67275 Murray re
21	18.6	21.9	60	15 AEL69636	Ael69636 Murray re
22	18.6	21.9	65	6 ABN27281	Abn27281 Rat splic
23	18.6	21.9	78	2 AAT21804	Aat21804 Human gen
24	18.4	21.6	43	2 AAQ85150	Aaq85150 Ureaplas
25	18.4	21.6	43	2 AAQ85118	Aaq85118 Ureaplas
26	18.4	21.6	43	2 AAQ85119	Aaq85119 Ureaplas
27	18.4	21.6	43	2 AAQ85138	Aaq85138 Ureaplas
28	18.4	21.6	50	15 AEG86030	Aeg86030 Hematolog
29	18.4	21.6	54	15 AEJ57607	Aej57607 SARS coro
30	18.4	21.6	54	15 AEK13577	Aek13577 SARS coro
31	18.4	21.6	69	2 AAT88275	Aat88275 M17 synth
32	18.4	21.6	70	14 ADY93938	Ady93938 Codon opt
33	18.4	21.6	70	14 ADY93993	Ady93993 Codon opt
34	18.4	21.6	85	6 ABL50273	Ab150273 Chimeric
35	18.2	21.4	40	13 ADU09560	Adu09560 Amidase p
36	18.2	21.4	40	15 AEF80899	Aef80899 Comamonas
37	18.2	21.4	40	15 AEH87849	Aeh87849 C. testos
38	18.2	21.4	59	10 ACD95017	Acd95017 Human col
39	18.2	21.4	60	6 ABN32231	Abn32231 Human spl
40	18.2	21.4	60	14 AED19289	Aed19289 E. coli s
41	18.2	21.4	65	6 ABN58415	Abn58415 Mouse spl
42	18.2	21.4	65	6 ABN30268	Abn30268 Rat splic
43	18.2	21.4	65	15 AEI67892	Aei67892 DNA encod
44	18	21.2	37	11 ADO70341	Ado70341 PCR prime
45	18	21.2	40	6 ABN88696	Abn88696 E2F aptam

## ALIGNMENTS

RESULT 1  
ABZ02865  
ID ABZ02865 standard; DNA; 50 BP.

AC ABZ02865;  
XX  
XX 09-JAN-2003 (first entry)  
DT

XX Human leukocyte gene expression profiling probe SEQ ID NO 2856.

DE T7; leukocyte; gene expression profiling; allograft rejection;  
XX atherosclerosis; congestive heart failure; systemic lupus erythematosus;  
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;  
KW ss.

XX Homo sapiens.

XX WO200257414-A2.

XX 25-JUL-2002.

XX 22-OCT-2001; 2001WO-US047856.

XX 20-OCT-2000; 2000US-0241994P.

XX 08-JUN-2001; 2001US-0296764P.

XX (BIOC-) BIOCARDIA INC.

XX Wohlgenuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;

XX Ly N, Woodward R, Queternous T, Johnson F;

XX WPI; 2002-636525/68.

XX New system for leukocyte expression profiling, diagnosing a disease, or

XX monitoring (the rate of) progression of a disease, e.g. atherosclerosis

XX or congestive heart failure, comprises diagnostic oligonucleotides.

XX Claim 1; Page 418; Opp; English.

XX The invention relates to a system for detecting gene expression, which





RESULT 4  
ABN36304  
ID ABN36304 standard; DNA; 60 BP.  
XX AC ABN36304;  
XX AC ABN36304;  
DT 15-JUL-2002 (first entry)  
XX Human spliced transcript detection oligonucleotide SEQ ID NO:9052.  
XX Human; mouse; rat; splice transcript; detection; RNA transcript;  
KW splice variant; transcriptome; oligonucleotide library; ss.  
XX Homo sapiens.  
XX WO200210449-A2.  
XX PN 07-FEB-2002.  
PD 20-JUL-2001; 2001WO-IB001903.  
XX PF 28-JUL-2000; 2000US-0221607P.  
XX PR 02-MAY-2001; 2001US-0287724P.  
XX PA (COMP-) COMPUGEN INC.  
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
XX WPI; 2002-257383/30.  
XX New oligonucleotide libraries comprising oligonucleotides which  
PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
PT genome, useful for detecting tissue-, pathology-, and developmental-  
PT specific genes.  
XX Example 1; SEQ ID NO 9052; 47pp; English.  
XX  
CC The present invention describes oligonucleotide libraries for detecting  
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
CC )transcriptome comprises messenger RNAs transcribed from multiple  
CC transcription units that populate a genome. The library comprises several  
CC oligonucleotides, each capable of hybridising selectively to a set of  
CC messenger RNAs transcribed from a given transcription unit of the genome,  
CC which encodes one or more messenger RNA splice variants. The  
CC oligonucleotide libraries are useful for detecting mRNAs from a  
CC biological sample, in expression profiling studies, in qualitatively or  
CC quantitatively characterising the corresponding transcriptome, and in  
CC detecting RNA transcripts and splice variants of human or animal  
CC transcriptomes. The libraries may also be used as specialised mini  
CC libraries to detect transcripts of a sub-transcriptome under a particular  
CC biological or pathological state, and so allowing the detection of tissue  
CC - and pathology-specific genes such as those genes only expressed in  
CC specific tissue under a specific pathological condition; to detect  
CC developmental specific genes; and to detect RNA transcripts and splice  
CC variants of a transcriptome of a patient suffering from a particular  
CC disorder. ABN27253 to ABN39589 represent oligonucleotide sequences from  
CC rats, humans and mice, which are used in the exemplification of the  
CC present invention. N.B. The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 60 BP; 12 A; 9 C; 21 G; 18 T; 0 U; 0 Other;  
SQ  
Query Match 23.5%; Score 20; DB 6; Length 60;  
Best Local Similarity 38.9%; Pred. No. 2.2e+03;  
Matches 14; Conservative 12; Mismatches 10; Indels 0; Gaps 0  
QY 43 GUUGGAAGGGCGGUUGCUUCUUGUUUCUGGAUGCA 78  
DB 25 GTTGGAAGAGCGGATTGCTTGGTATTCTGCTTCA 60



quantitatively characterising the corresponding transcriptome, and in  
detecting RNA transcripts and splice variants of human or animal  
transcriptomes. The libraries may also be used as specialised mini  
libraries to detect transcripts of a sub-transcriptome under a particular  
biological or pathological state, and so allowing the detection of tissue  
- and pathology-specific genes such as those genes only expressed in  
specific tissue under a specific pathological condition; to detect  
developmental specific genes; and to detect RNA transcripts and splice  
variants of a transcriptome of a patient suffering from a particular  
disorder. ABN27253 to ABN3589 represent oligonucleotide sequences from  
rats, humans and mice, which are used in the exemplification of the  
present invention. N.B. The sequence data for this patent did not form  
part of the printed specification, but was obtained in electronic format  
directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Query Match	22.6%	Score	19.2	DB	6	Length	65
Best Local Similarity	41.7%	Pred. NO.	4.5e+03				
Matches	20	Conservative	10	Mismatches	18	Indels	0
						Gaps	0

[illegible]

RESULT 9  
ADM95921/c  
ID ADM95921 standard; DNA; 80 BP.  
XX  
XX  
AC ADM95921;  
XX  
XX  
DT 01-JUL-2004 (first entry)  
XX  
XX  
DE Rat antisense oligonucleotide #814.

Rat; antisense oligonucleotide; ss; antisense RNA production; oncogenes  
 tumour suppressor; cell cycle regulator; ion channel protein;  
 transport protein; intracellular signal transduction;  
 transcription factor; DNA-binding protein;  
 cell-cell communication protein; stress response gene;  
 apoptosis related gene; growth factor; chemokine; interleukin;  
 interferon; hormone; neurotransmitter; cell surface antigen;  
 cell adhesion molecule.

07-MAR-2002; 2002US-0362823P.  
(CHEN/) CHENCHIK A.

The invention relates to a standardising control for RNA samples to be tested on non-control gene sequences on nucleic acid arrays, useful for producing a population of distinct antisense RNA molecules from an initial population of distinct mRNA molecules.

Disclosure; SEQ ID NO 814; 282pp; English.

CC oncogenes, genes encoding tumour suppressors, cell cycle regulators, ion  
 CC channel proteins, transport proteins, intracellular signal transduction  
 CC modulator and effector factors, transcription factors, DNA-binding  
 CC proteins, receptors or cell-cell communication proteins, stress response  
 CC genes, apoptosis related genes, DNA synthesis/recombination/repair genes  
 CC and DNA-binding proteins. The genes encoding receptors comprise receptors  
 CC for growth factors, chemokines, interleukins, interferons, hormones,  
 CC neurotransmitters, cell surface antigens or cell adhesion molecules. The  
 CC genes encoding cell-cell communication proteins comprise growth factors,  
 CC cytokines, chemokines, interleukins, interferons or hormones. The  
 CC standardising control for RNA samples to be tested on non-control gene  
 CC sequences on nucleic acid arrays is useful for producing a population of  
 CC distinct antisense RNA molecules from an initial population of distinct  
 CC mRNA molecules. This sequence represents an antisense oligonucleotide of  
 CC the invention.

XX SQ Sequence 80 BP; 21 A; 21 C; 14 G; 24 T; 0 U; 0 Other;  
 Query Match 22.6%; Score 19.2; DB 12; Length 80;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+03;  
 Matches 15; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

Oy 33 GCGUCCCAAGUGAGGCGUUGUCUGUUUCUG 72  
 |||||:|||||:|||||:|||||:|||||:  
 Db 52 GAGTCTCATATTCAGACCTCGTGTCTATTCTG 13

RESULT 10  
 ABZ05513  
 ID ABZ05513 standard; DNA; 50 BP.  
 XX AC ABZ05513;  
 XX DT 09-JAN-2003 (first entry)  
 XX DE Human leukocyte gene expression profiling probe SEQ ID NO 5504.  
 XX KW T7; leukocyte; gene expression profiling; allograft rejection;  
 KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;  
 KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;  
 KW SS.

OS Homo sapiens.  
 XX WO200257414-A2.  
 XX PD 25-JUL-2002.  
 XX PF 22-OCT-2001; 2001WO-US047856.  
 XX PR 20-OCT-2000; 2000US-0241994P.  
 XX PR 08-JUN-2001; 2001US-0296764P.  
 XX PA (BIOC-) BIOCARDIA INC.  
 XX PI Wohlgenuth J, Fry K, Matuk G, Altman P, Prentice J, Phillips J;  
 PI Ly N, Woodward R, Quettermous T, Johnson F;  
 XX WPI; 2002-636525/68.

XX PT New system for leukocyte expression profiling, diagnosing a disease, or  
 PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis  
 PT or congestive heart failure, comprises diagnostic oligonucleotides.  
 XX PS Claim 1; Page 506; Opp; English..  
 XX CC The invention relates to a system for detecting gene expression, which  
 CC comprises one or two isolated DNA molecules that detect expression of a  
 CC gene, where the gene corresponds to any of 8143 oligonucleotides  
 CC (ABZ0010-ABZ08152) each having 50 base pairs (bp). The system is useful  
 CC for leukocyte expression profiling. It is particularly useful for  
 CC diagnosing a disease, monitoring (rate of) progression of a disease,  
 CC predicting therapeutic outcome, determining prognosis for a patient,

CC predicting disease complications in an individual or monitoring response  
 CC to treatment in an individual. The diseases include cardiac allograft  
 CC rejection, kidney allograft rejection, liver allograft rejection,  
 CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,  
 CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection  
 XX SQ Sequence 50 BP; 14 A; 6 C; 17 G; 13 T; 0 U; 0 Other;

Query Match 22.4%; Score 19; DB 6; Length 50;  
 Best Local Similarity 41.9%; Pred. No. 4.9e+03;  
 Matches 18; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

Oy 38 CCCAAGUGGAGGCGGCUUGUCUGUUUCUGGAGGCGAGA 80  
 |||||:|||||:|||||:|||||:|||||:  
 Db 2 CCTCAGTACAAAGGGGCGCTTGAAGTGTGTGCTGAATA 44

RESULT 11  
 AEC75978/c  
 ID AEC75978 standard; DNA; 60 BP.  
 XX AC AEC75978;  
 XX DT 01-DEC-2005 (first entry)  
 XX DE Cancer prognosis associated genetic marker SEQ ID NO 140.  
 XX KW prognosis; genetic marker; breast tumor; cytostatic;  
 KW gynecology and obstetrics; neoplasm; neurodegenerative disease;  
 KW neuroprotective; neurological disease; autoimmune disease;  
 KW immunosuppressive; immune disorder; diabetes; antidiabetic;  
 KW endocrine disease; gastrointestinal disease; metabolic disorder; obesity;  
 KW anorectic; nutritional disorder; estrogen receptor negative; ds.

OS Homo sapiens.  
 XX WO2005086891-A2.  
 XX PD 22-SEP-2005.  
 XX PF 07-MAR-2005; 2005WO-US007894.  
 XX PR 05-MAR-2004; 2004US-0550810P.  
 XX PR 24-AUG-2004; 2004US-0604076P.  
 XX PR 04-FEB-2005; 2005US-0650401P.  
 XX PA (ROSE-) ROSETTA INPHARMATICS LLC.  
 XX PA (NECA-) NETHERLANDS CANCER INST.

XX PI Dai H, Vant Veer LJ, Lamb J, Stoughton R, Friend SH, He Y;  
 XX WPI; 2005-676249/69.  
 XX PT Method of identifying informative genes or marker for breast cancer,  
 PT involves identifying set of genes or marker informative for condition, in  
 PT each classes such that set of genes in each classes is unique to class  
 PT relative to other classes.

XX PS Disclosure; SEQ ID NO 140; 280pp; English.  
 XX CC The invention describes a prognostic method. Samples are classified based  
 CC on the phenotypic or genotypic characteristics of the disease condition  
 CC e.g. cancer, into several classes. A set of genes or marker informative  
 CC for the condition is identified within each classes, such that the set of  
 CC genes or markers within each classes is unique to the class relative to  
 CC the other classes. Also described are: a method of classifying an  
 CC individual with a condition having good prognosis or poor prognosis; a  
 CC method of classifying breast cancer patient having good prognosis or poor  
 CC prognosis; a method of assigning individual to several categories in  
 CC clinical trial; a method of identifying set of genes informative for  
 CC condition; a method of predicting breast cancer patient with good  
 CC prognosis or poor prognosis; a microarray; and a microarray kit. The  
 CC method is useful for identifying informative genes or marker for disease

CC such as breast cancer, diabetes, autoimmune, neurodegenerative disorder  
CC and obesity. The method provides improved prognostic process to provide  
CC appropriate course of prophylaxis and therapy. This sequence represents a  
CC genetic marker associated with cancer prognosis.

XX SQ Sequence 60 BP; 13 A; 16 C; 15 G; 16 T; 0 U; 0 Other;

Query Match 22.4%; Score 19; DB 14; Length 60;  
Best Local Similarity 51.2%; Pred. No. 5.2e+03;  
Matches 22; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 1 GGGUUAUCUGCAACUGAGAGGGGCGUGUUAAGGCGUCCCAAG 43  
|| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
Db 55 GGTATTATTCATCTTCAGGGGTGGAAGAGCTGTCCCAAG 13

## RESULT 12

AEJ81361/c  
ID AEJ81361 standard; cDNA; 60 BP.

XX AC AEJ81361;

XX DT 19-OCT-2006 (first entry)

XX DE Human cDNA diagnostic/prognostic for breast cancer NM\_004207 #2.

XX KW Diagnosis; prognosis; ss; breast tumor; cancer; cytostatic; neoplasm;  
XX KW DNA microarray; gene expression; tumor marker.

XX OS Homo sapiens.

XX PN WO2006084272-A2.

XX PD 10-AUG-2006.

XX PF 06-FEB-2006; 2006WO-US004280.

XX PR 04-FEB-2005; 2005US-0650365P.

XX PA (ROSE-) ROSETTA INPHARMATICS LLC.

XX PA (MERI ) MERCK & CO INC.

XX PI Dai H, Friend SH, Deutsch P;

XX DR WPI; 2006-613101/63.

XX PT Predicting responsiveness of breast cancer patient to chemotherapy based  
XX on patient's cellular constituent profile, comprises measurement of  
XX cellular constituents, estrogen receptor (ER) level and ER level relative  
XX to patient's age.

XX PS Disclosure; SEQ ID NO 140; 349pp; English.

XX CC The invention relates to predicting responsiveness of a breast cancer  
XX patient to chemotherapy, comprising predicting the patient to exhibit  
XX enhanced response to chemotherapy as compared to patients in the general  
XX population of breast cancer patients if the cellular constituent profile  
XX is a poor prognosis profile, and the estrogen receptor (ER) level is ER+  
XX, and the ER level relative to patient's age (ER/AGE) is low. Also  
XX included are selecting a patient for enrollment in a clinical trial of a  
XX drug for treating breast cancer (based on the cellular constituent  
XX profile, ER level and an ER/AGE), identifying a breast cancer patient as  
XX a good or poor candidate for chemotherapy (based on the cellular  
XX constituent profile, ER level and an ER/AGE) and a computer system and  
XX program for carrying out the predicting, selecting and identifying  
XX methods. In the predicting method, the ER level is determined by  
XX measuring an expression level of a gene encoding the ER in the patient  
XX relative to expression level of the gene in the control sample. The gene  
XX encoding the ER is the ERalpha gene. The estrogen receptor level is  
XX measured by an oligonucleotide probe. The chemotherapy is carried out  
XX using cyclophosphamide, methotrexate and 5-fluorouracil. The method is  
XX useful for predicting responsiveness of a breast cancer patient to  
XX chemotherapy based on measurement of cellular constituents, ER level and

CC ER/AGE. The cellular constituent profile is used to determine patients  
CC suitable for clinical trials of a drug for treating breast cancer and  
CC determining if the patient is a good or poor candidate for chemotherapy.  
CC The method enables improved and high sensitive prediction of the  
CC responsiveness of a breast cancer patient to chemotherapy. The present  
CC sequence is a fragment of a human cDNA whose differential expression  
CC level makes it a candidate for the cellular constituent profile.

XX SQ Sequence 60 BP; 13 A; 16 C; 15 G; 16 T; 0 U; 0 Other;  
Query Match 22.4%; Score 19; DB 15; Length 60;  
Best Local Similarity 51.2%; Pred. No. 5.2e+03;  
Matches 22; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 1 GGGUUAUCUGCAACUGAGAGGGGCGUGUUAAGGCGUCCCAAG 43  
|| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
Db 55 GGTATTATTCATCTTCAGGGGTGGAAGAGCTGTCCCAAG 13

## RESULT 13

AAL30539

ID AAL30539 standard; DNA; 50 BP.

XX AC AAL30539;

XX DT 24-JAN-2002 (first entry)

XX DE Human SNP oligonucleotide #3747.

XX KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
XX KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
XX KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
XX KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
XX KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
XX KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
XX KW multifactorial disease; autoimmune disease; infection;  
XX KW nervous system disease; ss.

XX OS Homo sapiens.

XX PN WO200147944-A2.

XX PD 05-JUL-2001.

XX PF 28-DEC-2000; 2000WO-US035498.

XX PR 28-DEC-1999; 99US-0173419P.

XX PR 27-DEC-2000; 2000US-00173419.

XX PA (CURA-) CURAGEN CORP.

XX PI Shimkets RA, Leach M;

XX DR WPI; 2001-465210/50.

XX CC Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
XX oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
XX autoimmune diseases and infections.

XX Claim 1; Page 2462; 4143pp; English.

XX CC The present invention relates to oligonucleotides encoding polymorphic  
XX variants of proteins related to amylases, amyloid proteins, angiotensin,  
XX apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
XX histones, kinases, colony stimulating factors, complement related  
XX proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-  
XX protein coupled receptors and thioesterases. The present sequence is one  
XX such oligonucleotide. The oligonucleotides and the peptides encoded by  
XX them may be used in the prevention, diagnosis and treatment of diseases  
XX associated with inappropriate expression of the proteins listed above.  
XX Disorders that may be prevented, diagnosed and/or treated include  
XX multifactorial diseases with a genetic component, such as autoimmune  
XX diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,

CC systemic lupus erythromatosus and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukaemia), diseases of the nervous system and an infection of pathogenic  
CC organisms  
SQ Sequence 50 BP; 12 A; 9 C; 21 G; 8 T; 0 U; 0 Other;  
Query Match 22.1%; Score 18.8; DB 4; Length 50;  
Best Local Similarity 56.5%; Pred. No. 5.9e+03;  
Matches 26; Conservative 3; Mismatches 17; Indels 0; Gaps 0;  
QY 9 UGCAACUGAGAGGGGCGUGUUAAGCGGCCUCCCAAGUUGGAAGGGCG 54  
DB 4 TGCACCTTACGGGGCTGGAGAGCGCTGGATAAGACAGAGGGCG 49  
RESULT 14  
AAL30538  
ID AAL30538 standard; DNA; 50 BP.  
XX  
AC AAL30538;  
XX  
24-JAN-2002 (first entry)  
XX  
DE Human SNP oligonucleotide #3746.  
XX  
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KW neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;  
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease; ss.  
XX  
OS Homo sapiens.  
XX  
FN WO200147944-A2.  
XX  
PD 05-JUL-2001.  
XX  
28-DEC-2000; 2000WO-US035498.  
XX  
28-DEC-1999; 99US-0173419P.  
PR 27-DEC-2000; 2000US-00173419.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Shimkets RA, Leach M;  
XX  
WPI; 2001-465210/50.  
XX  
Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
PT autoimmune diseases and infections.  
XX  
PS Claim 1; Page 2462; 4143pp; English.  
XX  
The present invention relates to oligonucleotides encoding polymorphic  
CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
CC histones, kinases, colony stimulating factors, complement related  
CC proteins, cytochromes, kinesin, cytokines, interferons, interleukins, G-  
CC protein coupled receptors and thioesterases. The present sequence is one  
CC such oligonucleotide. The oligonucleotides and the peptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of the proteins listed above.  
CC Disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC systemic lupus erythromatosus and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukaemia), diseases of the nervous system and an infection of pathogenic

CC organisms  
XX  
SQ Sequence 50 BP; 12 A; 10 C; 20 G; 8 T; 0 U; 0 Other;  
Query Match 22.1%; Score 18.8; DB 4; Length 50;  
Best Local Similarity 56.5%; Pred. No. 5.9e+03;  
Matches 26; Conservative 3; Mismatches 17; Indels 0; Gaps 0;  
QY 9 UGCAACUGAGAGGGGCGUGUUAAGCGGCCUCCCAAGUUGGAAGGGCG 54  
DB 5 TGCACCTTACGGGGCTGGAGAGCGCTGGATAAGACAGAGGGCG 50  
RESULT 15  
AAX33875/c  
ID AAX33875 standard; RNA; 60 BP.  
XX  
AC AAX33875;  
XX  
25-JUN-1999 (first entry)  
XX  
DE HPV-16 inhibitor.  
XX  
KW HPV-16; inhibitor; antisense oligonucleotide; E6/E7 gene; human;  
KW keratinocyte; cervical cell; cervical tumour; ss.  
XX  
OS Synthetic.  
OS Human papillomavirus type 16.  
XX  
PN WO9913071-A1.  
XX  
PD 18-MAR-1999.  
XX  
PF 03-SEP-1998; 98WO-US018320.  
XX  
PR 05-SEP-1997; 97US-00929140.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Dipaolo J, Alvarez-Salas L;  
XX  
WPI; 1999-243727/20.  
XX  
New antisense oligonucleotide analogs for inhibiting growth of cervical  
PT tumors.  
XX  
PS Disclosure; Page 7; 40pp; English.  
XX  
This sequence represents an antisense oligonucleotide of the invention.  
CC The antisense oligonucleotide analogs (ONs) have a sequence complementary  
CC to a sequence of nucleotides 415-445 of human papilloma virus-16 (HPV-  
CC 16). The antisense ONs can be used to inhibit expression of HPV gene  
CC E6/E7 in living cells, preferably human keratinocytes or human cervical  
CC cells. They bind to E6/E7 mRNA in the cell, prevent mRNA translation and  
CC promote mRNA degradation by intracellular RNase H. They can be used for  
CC preventing transformation of living cells by HPV. The antisense ONs are  
CC used particularly for inhibiting the growth of cervical tumours  
XX  
SQ Sequence 60 BP; 14 A; 15 C; 15 G; 0 T; 16 U; 0 Other;  
Query Match 22.1%; Score 18.8; DB 2; Length 60;  
Best Local Similarity 41.3%; Pred. No. 6.2e+03;  
Matches 19; Conservative 10; Mismatches 17; Indels 0; Gaps 0;  
QY 29 UAGAGGCGUCCCAAGUUGGAAGGGCGGUUUGCUUUGCUUUUUGGA 74  
DB 49 TACCACGGACCGAAGTCCGTCGACGCTCTGCTGCTCTCTCTGAA 4  
Search completed: June 19, 2007, 16:30:34  
Job time : 317 secs

Result No.	Query			Description		
	Score	Match	Length	ID	DB	
1	21.4	25.2	50	3	US-10-131-827-2856	Sequence 2856, Ap
2	21.4	25.2	50	5	US-10-131-831-2856	Sequence 2856, Ap
3	19.8	23.3	83	3	US-09-621-976-13389	Sequence 13389, A
4	19	22.4	50	3	US-10-131-827-5504	Sequence 5504, Ap
5	19	22.4	50	5	US-10-131-831-5504	Sequence 5504, Ap
C 6	18.8	22.1	61	3	US-08-929-140-9	Sequence 9, Appli
C 7	18.8	22.1	61	3	US-09-560-579A-9	Sequence 9, Appli
C 8	18.6	21.9	68	2	US-08-981-663-59	Sequence 59, Appl
C 9	18.6	21.9	76	2	US-08-981-663-61	Sequence 61, Appl
C 10	18.6	21.9	76	2	US-08-981-663-62	Sequence 62, Appl
C 11	18.6	21.9	76	2	US-08-981-663-65	Sequence 65, Appl
12	18.6	21.9	76	2	US-08-981-663-66	Sequence 66, Appl
13	18.4	21.6	43	3	US-08-109-037-22	Sequence 22, Appl
C 14	18.4	21.6	43	3	US-08-109-037-55	Sequence 55, Appl
C 15	18.4	21.6	43	3	US-08-109-037-56	Sequence 56, Appl
C 16	18.4	21.6	43	3	US-08-109-037-57	Sequence 57, Appl
17	18.4	21.6	69	3	US-09-025-769B-336	Sequence 336, App
18	18.4	21.6	69	3	US-09-490-070A-336	Sequence 336, App
19	18.4	21.6	69	3	US-09-490-133-336	Sequence 336, App
20	18.4	21.6	69	3	US-09-490-324-336	Sequence 336, App
21	17.8	20.9	50	3	US-10-131-827-2558	Sequence 2558, Ap
22	17.8	20.9	50	3	US-10-131-827-6041	Sequence 6041, Ap
23	17.8	20.9	50	3	US-10-131-827-6334	Sequence 6334, Ap



FILE REFERENCE: 506612000121  
 CURRENT APPLICATION NUMBER: US/10/131.831  
 PRIOR FILING DATE: 2002-08-05  
 PRIOR APPLICATION NUMBER: US 10/006,290  
 PRIOR FILING DATE: 2001-10-22  
 PRIOR APPLICATION NUMBER: US 60/296,764  
 PRIOR FILING DATE: 2001-06-08  
 NUMBER OF SEQ ID NOS: 9190  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 2856  
 LENGTH: 50  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-131-831-2856

Query Match 25.2%; Score 21.4; DB 5; Length 50;  
 Best Local Similarity 41.0%; Pred. No. 1.2e+02;  
 Matches 16; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

Qy 42 AGUUGAAGGCGGCUUUCUGUUGUUGAUGCAGA 80  
 Db 1 AGTCCCAAGGCTGTTTGTACTTTTCTCCATGAATA 39

RESULT 3  
 US-09-621-976-13389  
 Sequence 13389, Application US/09621976  
 Patent No. 6639063

GENERAL INFORMATION:  
 APPLICANT: Dumas Milne Edwards, J.B.  
 APPLICANT: Jobert, S.  
 APPLICANT: Giordano, J.Y.  
 TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
 FILE REFERENCE: GENSET.054PR2  
 CURRENT APPLICATION NUMBER: US/09/621.976  
 CURRENT FILING DATE: 2000-07-21  
 NUMBER OF SEQ ID NOS: 19335  
 SOFTWARE: Patent.pm  
 SEQ ID NO 13389  
 LENGTH: 83  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-621-976-13389

Query Match 23.3%; Score 19.8; DB 3; Length 83;  
 Best Local Similarity 43.7%; Pred. No. 5.9e-02;  
 Matches 31; Conservative 8; Mismatches 32; Indels 0; Gaps 0;

Qy 2 GGUAUCUGCAACUGAGAGGCGGCUUUAAGCGUCCCAAGUUGAAGGCGGCUUUGCU 61  
 Db 6 GGGCACCTGCTAGAGGTAGGTGGAACTCCATCCCATGACGACGGGCTCATCTCT 65

Qy 62 UCUGUUUUCUG 72  
 Db 66 GCTGCTCCCG 76

RESULT 4  
 US-10-131-827-5504  
 Sequence 5504, Application US/10131827  
 Patent No. 6905827

GENERAL INFORMATION:  
 APPLICANT: Wohlgemuth, Jay  
 APPLICANT: Fry, Kirk  
 APPLICANT: Woodward, Robert  
 APPLICANT: Ly, Ngoc  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE  
 FILE REFERENCE: 506612000120  
 CURRENT APPLICATION NUMBER: US/10/131,827  
 CURRENT FILING DATE: 2002-09-06  
 PRIOR APPLICATION NUMBER: US 10/006,290  
 PRIOR FILING DATE: 2001-10-22

PRIOR APPLICATION NUMBER: US 60/296,764  
 PRIOR FILING DATE: 2001-06-08  
 NUMBER OF SEQ ID NOS: 9090  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 5504  
 LENGTH: 50  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-131-827-5504

Query Match 22.4%; Score 19; DB 3; Length 50;  
 Best Local Similarity 41.9%; Pred. No. 1e+03;  
 Matches 18; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

Qy 38 CCCAAGUUGAAGGCGGCUUUCUGUUGUUGAUGCAGA 80  
 Db 2 CCTCAGTACAAAGGGGCTTTGGAAGTCTTTGCTGCTGAATA 44

RESULT 5

US-10-131-831-5504  
 Sequence 5504, Application US/10131831  
 Patent No. 7026121

GENERAL INFORMATION:  
 APPLICANT: Wohlgemuth, Jay  
 APPLICANT: Fry, Kirk  
 APPLICANT: Woodward, Robert  
 APPLICANT: Ly, Ngoc  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING  
 TITLE OF INVENTION: TRANSPLANT REJECTION  
 FILE REFERENCE: 506612000121  
 CURRENT APPLICATION NUMBER: US/10/131,831  
 CURRENT FILING DATE: 2002-08-05  
 PRIOR APPLICATION NUMBER: US 10/006,290  
 PRIOR FILING DATE: 2001-10-22  
 PRIOR APPLICATION NUMBER: US 60/296,764  
 PRIOR FILING DATE: 2001-06-08  
 NUMBER OF SEQ ID NOS: 9190  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 5504  
 LENGTH: 50  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-131-831-5504

Query Match 22.4%; Score 19; DB 5; Length 50;  
 Best Local Similarity 41.9%; Pred. No. 1e+03;  
 Matches 18; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

Qy 38 CCCAAGUUGAAGGCGGCUUUCUGUUGUUGAUGCAGA 80  
 Db 2 CCTCAGTACAAAGGGGCTTTGGAAGTCTTTGCTGCTGAATA 44

RESULT 6

US-08-929-140-9/c  
 Sequence 9, Application US/08929140  
 Patent No. 6084090

GENERAL INFORMATION:  
 APPLICANT: Dipaolo, Joseph  
 APPLICANT: Alvarez-Salas, Luis  
 TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS INHIBITION  
 TITLE OF INVENTION: BY ANTISENSE OLIGONUCLEOTIDES  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Knobbe, Martens, Olson & Bear  
 STREET: 620 Newport Center Drive Sixteenth Flo  
 CITY: Newport Beach  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 92660  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette



```
;
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/929,140
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: NIH138.001A
; TELEPHONE: 714/760-0404
; TELEFAX: 714/760-9503
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-929-140-9

Query Match      22.1%; Score 18.8; DB 3; Length 61;
Best Local Similarity 41.3%; Pred. No. 1.3e+03;
Matches 19; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

Qy 29 UAAGCGUCCCAAGUUGGAGCGCGUUGUCUUGUUCUGGA 74
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 49 TACCACGACCGAAGTCGGTGTGACGCTCTGTTCTCTGAA 4

RESULT 7
US-09-560-579A-9/c
; Sequence 9, Application US/09560579A
; Patent No. 6277980
; GENERAL INFORMATION:
; APPLICANT: DiPaolo, Joseph
; ALVAREZ-SALAS, Luis
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS INHIBITION
; BY ANTISENSE OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive Sixteenth Flo
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/560,579A
; FILING DATE: 28-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/929,140
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: NIH138.001A
; TELEPHONE: 714/760-0404
; TELEFAX: 714/760-9503
; TELEX: <Unknown>
```

```
;
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-560-579A-9

Query Match      22.1%; Score 18.8; DB 3; Length 61;
Best Local Similarity 41.3%; Pred. No. 1.3e+03;
Matches 19; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

Qy 29 UAAGCGUCCCAAGUUGGAGCGCGUUGUCUUGUUCUGGA 74
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 49 TACCACGACCGAAGTCGGTGTGACGCTCTGTTCTCTGAA 4

RESULT 8
US-08-981-663-59/c
; Sequence 59, Application US/08981663
; Patent No. 5952176
; GENERAL INFORMATION:
; APPLICANT: MCCARTHY, THOMAS VALENTINE
; APPLICANT: VAUGHAN, PATRICK MARTIN
; TITLE OF INVENTION: GLYCOSYLASE MEDIATED DETECTION OF
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AT CANDIDATE LOCI
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,663
; FILING DATE: 08-JAN-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 1377-120P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 68 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
; US-08-981-663-59

Query Match      21.9%; Score 18.6; DB 2; Length 68;
Best Local Similarity 51.2%; Pred. No. 1.6e+03;
Matches 21; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 21 GGGCUGGUUAGCGGUCCCAAGUUGGAGCGCGCUUGUCU 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 43 GGGCTGTTTGGCCGCCACTACGTGTTAGTTCAGGATGCT 3
```

RESULT 9  
US-08-981-663-61/c  
; Sequence 61, Application US/08981663  
; Patent No. 5952176  
; GENERAL INFORMATION:  
; APPLICANT: MCCARTHY, THOMAS VALENTINE  
; APPLICANT: VAUGHAN, PATRICK MARTIN  
; TITLE OF INVENTION: GLYCOSYLASE MEDIATED DETECTION OF  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AT CANDIDATE LOCI  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP  
; STREET: P.O. Box 747  
; CITY: Falls Church  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/981.663  
; FILING DATE: 08-JAN-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SVENSSON, LEONARD R.  
; REGISTRATION NUMBER: 30,330  
; REFERENCE/DOCKET NUMBER: 1377-120P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; TELEX: 248345  
; INFORMATION FOR SEQ ID NO: 61:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 76 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Mycobacterium tuberculosis  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: 12  
; OTHER INFORMATION: /mod\_base= i  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: 22  
; OTHER INFORMATION: /mod\_base= i  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: 25  
; OTHER INFORMATION: /mod\_base= i  
US-08-981-663-61

Query Match 21.9%; Score 18.6; DB 2; Length 76;  
Best Local Similarity 51.2%; Pred. No. 1.7e+03;  
Matches 21; Conservative 6; Mismatches 14; Indels 0; Gaps 0;  
Qy 21 GGGCUGGUUAAGCGGCCCAAGUUGGAGGCGCGCUUUGCU 61  
Db 43 GGGCTGGTTTGGCCGCGCACTACGTGTAGGTACGATGCT 3

RESULT 10  
US-08-981-663-62  
; Sequence 62, Application US/08981663  
; Patent No. 5952176  
; GENERAL INFORMATION:  
; APPLICANT: MCCARTHY, THOMAS VALENTINE  
; APPLICANT: VAUGHAN, PATRICK MARTIN  
; TITLE OF INVENTION: GLYCOSYLASE MEDIATED DETECTION OF  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AT CANDIDATE LOCI  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP  
; STREET: P.O. Box 747  
; CITY: Falls Church  
; STATE: Virginia

COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/981.663  
FILING DATE: 08-JAN-1998  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: SVENSSON, LEONARD R.  
REGISTRATION NUMBER: 30,330  
REFERENCE/DOCKET NUMBER: 1377-120P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 76 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
ORIGINAL SOURCE:  
ORGANISM: Mycobacterium tuberculosis  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 12  
OTHER INFORMATION: /mod\_base= i  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 22  
OTHER INFORMATION: /mod\_base= i  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 25  
OTHER INFORMATION: /mod\_base= i  
US-08-981-663-62

Query Match 21.9%; Score 18.6; DB 2; Length 76;  
Best Local Similarity 58.5%; Pred. No. 1.7e+03;  
Matches 24; Conservative 3; Mismatches 14; Indels 0; Gaps 0;  
Qy 21 GGGCUGGUUAAGCGGCCCAAGUUGGAGGCGCGCUUUGCU 61  
Db 34 GGGCTGGTTTGGCCGCGCACTACGTGTAGGTACGATGCT 74

RESULT 11  
US-08-981-663-65/c  
; Sequence 65, Application US/08981663  
; Patent No. 5952176  
; GENERAL INFORMATION:  
; APPLICANT: MCCARTHY, THOMAS VALENTINE  
; APPLICANT: VAUGHAN, PATRICK MARTIN  
; TITLE OF INVENTION: GLYCOSYLASE MEDIATED DETECTION OF  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AT CANDIDATE LOCI  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP  
; STREET: P.O. Box 747  
; CITY: Falls Church  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

```
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/981.663
;; FILING DATE: 08-JAN-1998
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: SVENSSON, LEONARD R.
;; REGISTRATION NUMBER: 30,330
;; REFERENCE/DOCKET NUMBER: 1377-120P
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 205-8000
;; TELEFAX: (703) 205-8050
;; TELEX: 248345
;; INFORMATION FOR SEQ ID NO: 65:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 76 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: circular
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Mycobacterium tuberculosis
;; US-08-981-663-65

Query Match 21.9%; Score 18.6; DB 2; Length 76;
Best Local Similarity 51.2%; Pred. No. 1.7e+03;
Matches 21; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 21 GGGCUGGUUAAGGCGGCCCAAGUUGGAAGGCGCUUUGCU 61
Db 43 GGGCTGTTTGGCGGCCACTACGTGTTAGTCAGGATGCT 3

RESULT 12
US-08-981-663-66
; Sequence 66, Application US/08981663
; Patent No. 5952176
; GENERAL INFORMATION:
; APPLICANT: MCCARTHY, THOMAS VALENTINE
; APPLICANT: VAUGHAN, PATRICK MARTIN
; TITLE OF INVENTION: GLYCOSYLASE MEDIATED DETECTION OF
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AT CANDIDATE LOCI
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981.663
; FILING DATE: 08-JAN-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 1377-120P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 76 base pairs
```

```
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: circular
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: YES
;; ORIGINAL SOURCE:
;; ORGANISM: Mycobacterium tuberculosis
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: 12
;; OTHER INFORMATION: /mod_base= i
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: 22
;; OTHER INFORMATION: /mod_base= i
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: 25
;; OTHER INFORMATION: /mod_base= i
;; US-08-981-663-66

Query Match 21.9%; Score 18.6; DB 2; Length 76;
Best Local Similarity 58.5%; Pred. No. 1.7e+03;
Matches 24; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

Qy 21 GGGCUGGUUAAGGCGGCCCAAGUUGGAAGGCGCGCUUUGCU 61
Db 34 GGGCTGTTTGGCGGCCACUACUGGUAGGUCAGGAGCU 74

RESULT 13
US-08-109-037-22
; Sequence 22, Application 08/109037
; Patent No. 6093538
; GENERAL INFORMATION:
; APPLICANT: James J. Hogan, Diane L. McAllister,
; APPLICANT: Patricia Gordon, and Philip W. Hammond.
; TITLE OF INVENTION: NUCLEIC ACID PROBES
; TITLE OF INVENTION: TO UREAPLASMA
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: Wordperfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/109,037
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 07/879,685
; FILING DATE: May 6, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 193/121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43
```

```
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-109-037-22

Query Match      21.6%; Score 18.4; DB 3; Length 43;
Best Local Similarity 46.4%; Pred. No. 1.6e+03;
Matches 13; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 49 AGGCGCUUUGCUUUGUUUUGGAUG 76
Db 16 AGAGTGTGACTTCTGTGTCGGGATG 43

RESULT 14
US-08-109-037-55
; Sequence 55, Application 08/109037
; Patent No. 6093538
; GENERAL INFORMATION:
; APPLICANT: James J. Hogan, Diane L. McAllister,
; APPLICANT: Patricia Gordon, and Philip W. Hammond.
; TITLE OF INVENTION: NUCLEIC ACID PROBES
; TITLE OF INVENTION: TO UREAPLASMA
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: Wordperfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/109,037
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 07/879,685
; FILING DATE: May 6, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 193/121
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-109-037-55

Query Match      21.6%; Score 18.4; DB 3; Length 43;
Best Local Similarity 78.6%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 49 AGGCGCUUUGCUUUGUUUUGGAUG 76
Db 16 AGAGUGCUUGACUUCUGUGUUGGGAUG 43

RESULT 15
US-08-109-037-56/c
; Sequence 56, Application 08/109037
```

```
; Patent No. 6093538
; GENERAL INFORMATION:
; APPLICANT: James J. Hogan, Diane L. McAllister,
; APPLICANT: Patricia Gordon, and Philip W. Hammond.
; TITLE OF INVENTION: NUCLEIC ACID PROBES
; TITLE OF INVENTION: TO UREAPLASMA
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: Wordperfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/109,037
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 07/879,685
; FILING DATE: May 6, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 193/121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-109-037-56

Query Match      21.6%; Score 18.4; DB 3; Length 43;
Best Local Similarity 46.4%; Pred. No. 1.6e+03;
Matches 13; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 49 AGGCGCUUUGCUUUGUUUUGGAUG 76
Db 28 AGAGTGTGACTTCTGTGTCGGGATG 1

Search completed: June 19, 2007, 18:46:09
Job time : 655 secs
```

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 16:25:24 ; Search time 744 Seconds  
(without alignments)  
1403.829 Million cell updates/sec

Title: US-10-604-726A-6033  
Perfect score: 85  
Sequence: 1 ggguaucgacacagag.....uuuucgagcagaguccu 85

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 24367798

Minimum DB seq length: 0  
Maximum DB seq length: 85

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA Main.\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq.\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq.\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21.4	25.2	50	7	US-10-131-827-2856
2	20.8	24.5	76	3	US-09-899-575-73
3	20.2	23.8	66	11	US-10-310-914A-11123
4	20.2	23.8	68	11	US-10-310-914A-11331
5	20	23.5	60	3	US-09-908-975-9052
6	19.2	22.6	51	3	US-09-922-225A-51
7	19.2	22.6	65	3	US-09-908-975-26691
8	19.2	22.6	74	11	US-10-310-914A-11224
9	19.2	22.6	80	8	US-10-384-245-814
10	19	22.4	50	7	US-10-131-827-5504
11	19	22.4	50	16	US-11-175-859-53521
12	19	22.4	64	11	US-10-310-914A-10113
13	18.8	22.1	65	3	US-09-908-975-4025
14	18.8	22.1	70	10	US-10-957-432-458
15	18.8	22.1	73	11	US-10-310-914A-11927
16	18.8	22.1	83	11	US-10-310-914A-6916
17	18.6	21.9	50	16	US-11-175-859-26823

c	18	18.6	21.9	50	16	US-11-175-859-65785	Sequence 65785, A
c	19	18.6	21.9	60	3	US-09-908-975-7115	Sequence 7115, Appl
c	20	18.6	21.9	65	3	US-09-908-975-29	Sequence 29, Appl
c	21	18.4	21.6	69	11	US-10-834-937-336	Sequence 336, Appl
c	22	18.4	21.6	70	10	US-10-911-838-88	Sequence 88, Appl
c	23	18.4	21.6	70	10	US-10-911-838-143	Sequence 143, Appl
c	24	18.4	21.6	85	8	US-10-343-825A-4	Sequence 4, Appl
c	25	18.2	21.4	25	9	US-10-719-900-385230	Sequence 385230, A
c	26	18.2	21.4	25	9	US-10-719-900-453865	Sequence 453865, A
c	27	18.2	21.4	25	11	US-10-933-982-172709	Sequence 172709, A
c	28	18.2	21.4	26	8	US-10-403-161-111	Sequence 111, Appl
c	29	18.2	21.4	27	11	US-10-310-914A-166755	Sequence 166755, A
c	30	18.2	21.4	40	9	US-10-431-966-22	Sequence 22, Appl
c	31	18.2	21.4	40	11	US-10-977-893-22	Sequence 22, Appl
c	32	18.2	21.4	50	16	US-11-175-859-96339	Sequence 96339, A
c	33	18.2	21.4	60	3	US-09-908-975-4979	Sequence 4979, Appl
c	34	18.2	21.4	62	11	US-10-310-914A-15774	Sequence 15774, A
c	35	18.2	21.4	65	3	US-09-908-975-3016	Sequence 3016, Appl
c	36	18.2	21.4	65	3	US-09-908-975-31163	Sequence 31163, A
c	37	18	21.2	37	8	US-10-308-128-188	Sequence 188, Appl
c	38	18	21.2	40	3	US-09-963-827B-210	Sequence 210, Appl
c	39	18	21.2	50	16	US-11-175-859-92740	Sequence 92740, A
c	40	18	21.2	51	7	US-10-393-815-110	Sequence 110, Appl
c	41	18	21.2	60	3	US-09-908-975-11045	Sequence 11045, A
c	42	18	21.2	65	3	US-09-908-975-24811	Sequence 24811, A
c	43	18	21.2	72	8	US-10-313-783A-21	Sequence 21, Appl
c	44	17.8	20.9	24	10	US-10-750-185-13212	Sequence 13212, A
c	45	17.8	20.9	24	10	US-10-750-623-13212	Sequence 13212, A

## ALIGNMENTS

### RESULT 1

US-10-131-827-2856  
; Sequence 2856, Application US/10131827  
; Publication No. US20040009479A1  
; GENERAL INFORMATION:  
; APPLICANT: Wohlgemuth, Jay  
; APPLICANT: Fty. Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE  
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES  
; FILE REFERENCE: 50661200120  
; CURRENT APPLICATION NUMBER: US/10/131,827  
; CURRENT FILING DATE: 2002-09-06  
; PRIOR APPLICATION NUMBER: US 10/006,290  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 60/296,764  
; PRIOR FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 9090  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 2856  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-131-827-2856

Query Match 25.2%; Score 21.4; DB 7; Length 50;  
Best Local Similarity 41.0%; Pred. No. 9.9e+02;  
Matches 16; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

Qy 42 AGUUGAAGGCGGCUUCUUCUUCUUCUUCUUCUUCGAGCA 80

Db 1 AGTCCCAAGGCTGTTTGTCTACTGTTTCTCCATGAATA 39

### RESULT 2

US-09-899-575-73/c  
; Sequence 73, Application US/09899575  
; Publication No. US20030223961A1  
; GENERAL INFORMATION:

```
; APPLICANT: Zur Megede, Jan
; APPLICANT: Barnett, Susan W.
; APPLICANT: Egnelbrecht, Susan
; APPLICANT: van Rensburg, Estrelita Janse
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: P01631.102
; CURRENT APPLICATION NUMBER: US/09/899,575
; CURRENT FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 09/475,704
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
; LENGTH: 76
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV Type C
; OTHER INFORMATION: RevExon1 Wild Type
US-09-899-575-73

Query Match      24.5%; Score 20.8; DB 3; Length 76;
Best Local Similarity 41.1%; Pred. No. 1.8e+03;
Matches 23; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

Qy 15 UGAGAGGGCGUGUUAAGCGGCCCAAGUGGAGGCGGCUUUGCUUUCGUUUUC 70
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 71 TGATAGAGGATTTGATGATCTTACCACCTTGGAGGAGCGTTGCTGCTCTCC 16

RESULT 3
US-10-310-914A-11123
; Sequence 11123, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11123
; LENGTH: 66
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-11123

Query Match      23.8%; Score 20.2; DB 11; Length 66;
Best Local Similarity 68.3%; Pred. No. 2.9e+03;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 GGGUUAUCUGCAACUGAGAGGCGGUGUUAAGGCGUCCCA 41
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1 GGGUUAUGAGUGGUGAGAGGUGUUGGAGGAGGCCUCCCA 41

RESULT 4
US-10-310-914A-13331
; Sequence 1331, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
```

```
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13331
; LENGTH: 68
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-13331

Query Match      23.8%; Score 20.2; DB 11; Length 68;
Best Local Similarity 68.3%; Pred. No. 3e+03;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 GGGUUAUCUGCAACUGAGAGGCGGUGUUAAGGCGUCCCA 41
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 2 GGGUUAUGAGUGGUGAGAGGUGUUGGAGGAGGCCUCCCA 42

RESULT 5
US-09-908-975-9052
; Sequence 9052, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchaon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9052
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-9052

Query Match      23.5%; Score 20; DB 3; Length 60;
Best Local Similarity 38.9%; Pred. No. 3.4e+03;
Matches 14; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

Qy 43 GUUGAAGGCGCUUUGCUUUCUUGUUGUUGUUGUUGCA 78
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 25 GTTGGAGACGAGATTGCTTGTGTTATTCGTTC 60

RESULT 6
US-09-922-225A-51
; Sequence 51, Application US/09922225A
; Publication No. US20030104385A1
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; TITLE OF INVENTION: Nucleic Acids and Encoded Polypeptides
; TITLE OF INVENTION: Associated with Bipolar Disorder
; FILE REFERENCE: P-EA 4672
; CURRENT APPLICATION NUMBER: US/09/922,225A
; CURRENT FILING DATE: 2003-01-14
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-225A-51

Query Match      22.6%; Score 19.2; DB 3; Length 51;
Best Local Similarity 35.3%; Pred. No. 6.7e+03;
```



Search completed: June 19, 2007, 16:43:03  
Job time : 746 secs



us-10-604-726a-6033.sizlim85.rnpbm

Fri Jun 22 07:29:32 2007

Result No.	Score	Query Match	Length	DB ID	Description
C 1	32	37.6	32	11	US-10-536-560-175427
C 2	29	34.1	32	11	US-10-536-560-390712
C 3	21.4	25.2	50	7	US-10-990-275-2856
C 4	21.4	25.2	50	7	US-10-990-298-2856
C 5	21.4	25.2	50	8	US-10-006-290-2856
C 6	21.4	25.2	50	11	US-10-325-899-2856
C 7	20.8	24.5	64	19	US-11-130-645A-423399
C 8	20.8	24.5	64	19	US-11-130-645A-543086
C 9	20.6	24.2	62	19	US-11-130-645A-57160
C 10	20.6	24.2	63	19	US-11-130-645A-341409
C 11	20.2	23.8	64	19	US-11-130-645A-175103
C 12	20.2	23.8	64	19	US-11-130-645A-175103
C 13	20.2	23.8	64	19	US-11-130-645A-175103
C 14	20.2	23.8	64	19	US-11-130-645A-175103
C 15	20.2	23.8	64	19	US-11-130-645A-175103
C 16	20.2	23.8	64	19	US-11-130-645A-175103
C 17	20.2	23.8	64	19	US-11-130-645A-175103
C 18	20.2	23.8	64	19	US-11-130-645A-175103
C 19	20.2	23.8	64	19	US-11-130-645A-175103
C 20	20.2	23.8	64	19	US-11-130-645A-175103
C 21	20.2	23.8	64	19	US-11-130-645A-175103
C 22	20.2	23.8	64	19	US-11-130-645A-175103
C 23	20.2	23.8	64	19	US-11-130-645A-175103
C 24	20.2	23.8	64	19	US-11-130-645A-175103
C 25	20.2	23.8	64	19	US-11-130-645A-175103
C 26	20.2	23.8	64	19	US-11-130-645A-175103
C 27	20.2	23.8	64	19	US-11-130-645A-175103
C 28	20.2	23.8	64	19	US-11-130-645A-175103
C 29	20.2	23.8	64	19	US-11-130-645A-175103
C 30	20.2	23.8	64	19	US-11-130-645A-175103
C 31	20.2	23.8	64	19	US-11-130-645A-175103
C 32	20.2	23.8	64	19	US-11-130-645A-175103
C 33	20.2	23.8	64	19	US-11-130-645A-175103
C 34	20.2	23.8	64	19	US-11-130-645A-175103
C 35	20.2	23.8	64	19	US-11-130-645A-175103
C 36	20.2	23.8	64	19	US-11-130-645A-175103
C 37	20.2	23.8	64	19	US-11-130-645A-175103
C 38	20.2	23.8	64	19	US-11-130-645A-175103
C 39	20.2	23.8	64	19	US-11-130-645A-175103
C 40	20.2	23.8	64	19	US-11-130-645A-175103
C 41	20.2	23.8	64	19	US-11-130-645A-175103
C 42	20.2	23.8	64	19	US-11-130-645A-175103
C 43	20.2	23.8	64	19	US-11-130-645A-175103
C 44	20.2	23.8	64	19	US-11-130-645A-175103
C 45	20.2	23.8	64	19	US-11-130-645A-175103
C 46	20.2	23.8	64	19	US-11-130-645A-175103
C 47	20.2	23.8	64	19	US-11-130-645A-175103
C 48	20.2	23.8	64	19	US-11-130-645A-175103
C 49	20.2	23.8	64	19	US-11-130-645A-175103
C 50	20.2	23.8	64	19	US-11-130-645A-175103
C 51	20.2	23.8	64	19	US-11-130-645A-175103
C 52	20.2	23.8	64	19	US-11-130-645A-175103
C 53	20.2	23.8	64	19	US-11-130-645A-175103
C 54	20.2	23.8	64	19	US-11-130-645A-175103
C 55	20.2	23.8	64	19	US-11-130-645A-175103
C 56	20.2	23.8	64	19	US-11-130-645A-175103
C 57	20.2	23.8	64	19	US-11-130-645A-175103
C 58	20.2				

RESULT 2  
US-10-536-560-390712/c  
; Sequence 390712, Application US/10536560  
; Publication No. US20060257851A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD

; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
 ; TITLE OF INVENTION: GENES AND USES THEREOF  
 ; FILE REFERENCE: 06087.0300.PCUI3  
 ; CURRENT APPLICATION NUMBER: US/10/536,560  
 ; CURRENT FILING DATE: 2005-05-26  
 ; NUMBER OF SEQ ID NOS: 424571  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 390712  
 ; LENGTH: 32  
 ; TYPE: RNA  
 ; ORGANISM: Homo Sapiens  
 US-10-536-560-390712

Query Match. 34.1%; Score 29; DB 11; Length 32;  
 Best Local Similarity 55.2%; Pred. No. 2.9;  
 Matches 16; Conservative 13; Mismatches 0; Indels 0; Gaps 0;

Qy 57 UUGUUGUUUUUUGGAGUAGUCCU 85  
 Db 32 TTGCTTCTGTTTCTGGATGCAGATCCT 4

RESULT 3

US-10-990-275-2856  
 ; Sequence 2856, Application US/10990275  
 ; Publication No. US20070037166A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wohlgenuth, Jay  
 ; APPLICANT: Fry, Kirk  
 ; APPLICANT: Woodward, Robert  
 ; APPLICANT: Ly, Ngoc  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING  
 ; TITLE OF INVENTION: TRANSPLANT REJECTION  
 ; FILE REFERENCE: 50661200011  
 ; CURRENT APPLICATION NUMBER: US/10/990,275  
 ; CURRENT FILING DATE: 2004-11-15  
 ; PRIOR APPLICATION NUMBER: US 10/131,831  
 ; PRIOR FILING DATE: 2002-04-24  
 ; PRIOR APPLICATION NUMBER: US 10/006,290  
 ; PRIOR FILING DATE: 2001-10-22  
 ; PRIOR APPLICATION NUMBER: US 60/296,764  
 ; PRIOR FILING DATE: 2001-06-08  
 ; NUMBER OF SEQ ID NOS: 9190  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 2856  
 ; LENGTH: 50  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-990-275-2856

Query Match 25.2%; Score 21.4; DB 7; Length 50;  
 Best Local Similarity 41.0%; Pred. No. 1.7e+03;  
 Matches 16; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

Qy 42 AGUUGAAGGCGCUUGUUGUUGUUGUUGUUGAUGCAGA 80  
 Db 1 AGTCCCAAGGGTGTGTGTACTGTTTCTCCATGAATA 39

RESULT 4

US-10-990-298-2856  
 ; Sequence 2856, Application US/10990298  
 ; Publication No. US20070037167A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wohlgenuth, Jay  
 ; APPLICANT: Fry, Kirk  
 ; APPLICANT: Woodward, Robert  
 ; APPLICANT: Ly, Ngoc  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE  
 ; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES  
 ; FILE REFERENCE: 506612000110  
 ; CURRENT APPLICATION NUMBER: US/10/990,298  
 ; CURRENT FILING DATE: 2004-11-15

; PRIOR APPLICATION NUMBER: US 10/131,827  
 ; PRIOR FILING DATE: 2002-04-24  
 ; PRIOR APPLICATION NUMBER: US 10/006,290  
 ; PRIOR FILING DATE: 2001-10-22  
 ; PRIOR APPLICATION NUMBER: US 60/296,764  
 ; PRIOR FILING DATE: 2001-06-08  
 ; NUMBER OF SEQ ID NOS: 9090  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 2856  
 ; LENGTH: 50  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-990-298-2856

Query Match 25.2%; Score 21.4; DB 7; Length 50;  
 Best Local Similarity 41.0%; Pred. No. 1.7e+03;  
 Matches 16; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

Qy 42 AGUUGAAGGCGCUUGUUGUUGUUGUUGUUGAUGCAGA 80  
 Db 1 AGTCCCAAGGGTGTGTGTACTGTTTCTCCATGAATA 39

RESULT 5

US-10-006-290-2856  
 ; Sequence 2856, Application US/10006290  
 ; Publication No. US20070037144A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wohlgenuth, Jay  
 ; APPLICANT: Quetermou, Thomas  
 ; APPLICANT: Johnson, Frances  
 ; APPLICANT: Fry, Kirk  
 ; APPLICANT: Matcuk, George  
 ; APPLICANT: Prentice, James  
 ; APPLICANT: Phillips, Julie  
 ; APPLICANT: Woodward, Robert  
 ; APPLICANT: Ly, Ngoc  
 ; APPLICANT: Altman, Peter  
 ; TITLE OF INVENTION: LEUKOCYTE EXPRESSION PROFILING  
 ; FILE REFERENCE: 506612000100  
 ; CURRENT APPLICATION NUMBER: US/10/006,290  
 ; CURRENT FILING DATE: 2001-10-22  
 ; PRIOR APPLICATION NUMBER: US 60/241,994  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: US 60/296,764  
 ; PRIOR FILING DATE: 2001-06-08  
 ; NUMBER OF SEQ ID NOS: 8832  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 2856  
 ; LENGTH: 50  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-006-290-2856

Query Match 25.2%; Score 21.4; DB 8; Length 50;  
 Best Local Similarity 41.0%; Pred. No. 1.7e+03;  
 Matches 16; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

Qy 42 AGUUGAAGGCGCUUGUUGUUGUUGUUGUUGAUGCAGA 80  
 Db 1 AGTCCCAAGGGTGTGTGTACTGTTTCTCCATGAATA 39

RESULT 6

US-10-325-899-2856  
 ; Sequence 2856, Application US/10325899  
 ; Publication No. US20070031890A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wohlgenuth, Jay  
 ; APPLICANT: Fry, Kirk  
 ; APPLICANT: Ly, Ngoc  
 ; APPLICANT: Woodward, Robert  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING TRANSPLANT

```

RESULT 9
US-11-130-645A-57160
: Sequence 57160, Application US/11130645A
: Publication No. US20070050146A1
: GENERAL INFORMATION:
: APPLICANT: Bentwich, Itzhak
: APPLICANT: Amir, Avniel
: APPLICANT: Yael, Karov
: APPLICANT: Ranit, Aharonov
: TITLE OF INVENTION: Microrans and Uses Thereof
: FILE REFERENCE: 06087.0202.CPUS13
: CURRENT APPLICATION NUMBER: US/11/130,645A
: CURRENT FILING DATE: 2005-05-16
: PRIOR APPLICATION NUMBER: PCT/US05/16986
: PRIOR FILING DATE: 2005-05-14
: PRIOR APPLICATION NUMBER: US 10/709,577
: PRIOR FILING DATE: 2004-05-14

```

```
; PRIOR APPLICATION NUMBER: US 10/709,572
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/666,340
; PRIOR FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: US 60/665,094
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/662,742
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US 60/593,329
; PRIOR FILING DATE: 2005-01-06
; PRIOR APPLICATION NUMBER: US 60/593,081
; PRIOR FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: US 60/522,860
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/522,457
; PRIOR FILING DATE: 2004-10-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 57160
; LENGTH: 62
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-130-645A-57160

Query Match      24.2%; Score 20.6; DB 19; Length 62;
Best Local Similarity 67.4%; Pred. No. 3.4e+03;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 3 GUUAUCGCAACUGAGAGGGCGUGGUUAAGCGGUCCCAAGUU 45
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 17 GUGAUAAGAAACUUUGAAGGCGUAUUUAUCGCGUCCCAAGUU 59

RESULT 10
US-11-130-645A-341409
; Sequence 341409, Application US/11130645A
; Publication No. US20070050146A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Amir, Avniel
; APPLICANT: Yael, Karov
; TITLE OF INVENTION: Micronas and Uses Thereof
; FILE REFERENCE: 06087.0202.CPUS13
; CURRENT APPLICATION NUMBER: US/11/130,645A
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: PCT/US05/16986
; PRIOR FILING DATE: 2005-05-14
; PRIOR APPLICATION NUMBER: US 10/709,577
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/666,340
; PRIOR FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: US 60/665,094
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/662,742
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/593,329
; PRIOR FILING DATE: 2005-01-06
; PRIOR APPLICATION NUMBER: US 60/593,081
; PRIOR FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: US 60/522,860
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/522,457
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 341409
; LENGTH: 63
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-130-645A-341409

Query Match      24.2%; Score 20.6; DB 19; Length 63;
Best Local Similarity 67.4%; Pred. No. 3.4e+03;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 2 GUUAUCGCAACUGAGAGGGCGUGGUUAAGCGGUCCCAAGU 44
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 GUUCAUCCAGACAGAGAGGUGUGUACAGCGGCCCTUCAGU 43

RESULT 11
US-11-130-645A-175103
; Sequence 175103, Application US/11130645A
; Publication No. US20070050146A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Amir, Avniel
; APPLICANT: Yael, Karov
; TITLE OF INVENTION: Micronas and Uses Thereof
; FILE REFERENCE: 06087.0202.CPUS13
; CURRENT APPLICATION NUMBER: US/11/130,645A
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: PCT/US05/16986
; PRIOR FILING DATE: 2005-05-14
; PRIOR APPLICATION NUMBER: US 10/709,577
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 10/709,572
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/666,340
; PRIOR FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: US 60/665,094
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/662,742
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US 60/593,329
; PRIOR FILING DATE: 2005-01-06
; PRIOR APPLICATION NUMBER: US 60/593,081
; PRIOR FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: US 60/522,860
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/522,457
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 175103
; LENGTH: 64
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-130-645A-175103

Query Match      23.8%; Score 20.2; DB 19; Length 64;
Best Local Similarity 75.8%; Pred. No. 4.7e+03;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 42 AGUUGAAGGCGGUUGGUUUGUUUUUUGGA 74
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7 AUUUGAAUAAGAAUUGGUUUGGUUUUUGGA 39

RESULT 12
US-11-130-645A-275352
; Sequence 275352, Application US/11130645A
; Publication No. US20070050146A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Amir, Avniel
; APPLICANT: Yael, Karov
; TITLE OF INVENTION: Micronas and Uses Thereof
```

FILE REFERENCE: 06087.0202.CPUS13  
CURRENT APPLICATION NUMBER: US/11/130.645A  
CURRENT FILING DATE: 2005-05-16  
PRIOR APPLICATION NUMBER: PCT/US05/16986  
PRIOR FILING DATE: 2005-05-14  
PRIOR APPLICATION NUMBER: US 10/709,577  
PRIOR FILING DATE: 2004-05-14  
PRIOR APPLICATION NUMBER: US 10/709,572  
PRIOR FILING DATE: 2004-05-14  
PRIOR APPLICATION NUMBER: US 60/666,340  
PRIOR FILING DATE: 2005-03-30  
PRIOR APPLICATION NUMBER: US 60/665,094  
PRIOR FILING DATE: 2005-03-25  
PRIOR APPLICATION NUMBER: US 60/662,742  
PRIOR FILING DATE: 2005-03-17  
PRIOR APPLICATION NUMBER: US 60/593,329  
PRIOR FILING DATE: 2005-01-06  
PRIOR APPLICATION NUMBER: US 60/593,081  
PRIOR FILING DATE: 2004-12-08  
PRIOR APPLICATION NUMBER: US 60/522,860  
PRIOR FILING DATE: 2004-11-15  
PRIOR APPLICATION NUMBER: US 60/522,457  
PRIOR FILING DATE: 2004-10-04  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 760616  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 275352  
LENGTH: 64  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-130-645A-275352

Query Match 23.8%; Score 20.2; DB 19; Length 64;  
Best Local Similarity 75.8%; Pred. No. 4.7e+03;  
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 42 AGUUGGAAGCGCGCUUUGCUUUCUGUUGGA 74  
|||||  
Db 6 AUUUGGAUAAGGAUUGGCUUUCUGGA 38

RESULT 13  
US-11-130-645A-518054  
Sequence 518054, Application US/11130645A  
Publication No. US20070050146A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Itzhak  
APPLICANT: Amir, Avniel  
APPLICANT: Yael, Karov  
APPLICANT: Ranit, Aharonov  
TITLE OF INVENTION: Microtnas and Uses Thereof  
FILE REFERENCE: 06087.0202.CPUS13  
CURRENT APPLICATION NUMBER: US/11/130.645A  
CURRENT FILING DATE: 2005-05-16  
PRIOR APPLICATION NUMBER: PCT/US05/16986  
PRIOR FILING DATE: 2005-05-14  
PRIOR APPLICATION NUMBER: US 10/709,577  
PRIOR FILING DATE: 2004-05-14  
PRIOR APPLICATION NUMBER: US 10/709,572  
PRIOR FILING DATE: 2004-05-14  
PRIOR APPLICATION NUMBER: US 60/666,340  
PRIOR FILING DATE: 2005-03-30  
PRIOR APPLICATION NUMBER: US 60/665,094  
PRIOR FILING DATE: 2005-03-25  
PRIOR APPLICATION NUMBER: US 60/662,742  
PRIOR FILING DATE: 2005-03-17  
PRIOR APPLICATION NUMBER: US 60/593,329  
PRIOR FILING DATE: 2005-01-06  
PRIOR APPLICATION NUMBER: US 60/593,081  
PRIOR FILING DATE: 2004-12-08  
PRIOR APPLICATION NUMBER: US 60/522,860  
PRIOR FILING DATE: 2004-11-15  
PRIOR APPLICATION NUMBER: US 60/522,457

PRIOR FILING DATE: 2004-10-04  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 760616  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 518054  
LENGTH: 64  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-130-645A-518054

Query Match 23.8%; Score 20.2; DB 19; Length 64;  
Best Local Similarity 75.8%; Pred. No. 4.7e+03;  
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 42 AGUUGGAAGCGCGCUUUGCUUUCUGUUGGA 74  
|||||  
Db 6 AUUUGGAUAAGGAUUGGCUUUCUGGA 38

RESULT 14  
US-11-130-645A-520800  
Sequence 520800, Application US/11130645A  
Publication No. US20070050146A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Itzhak  
APPLICANT: Amir, Avniel  
APPLICANT: Yael, Karov  
APPLICANT: Ranit, Aharonov  
TITLE OF INVENTION: Microtnas and Uses Thereof  
FILE REFERENCE: 06087.0202.CPUS13  
CURRENT APPLICATION NUMBER: US/11/130.645A  
CURRENT FILING DATE: 2005-05-16  
PRIOR APPLICATION NUMBER: PCT/US05/16986  
PRIOR FILING DATE: 2005-05-14  
PRIOR APPLICATION NUMBER: US 10/709,577  
PRIOR FILING DATE: 2004-05-14  
PRIOR APPLICATION NUMBER: US 10/709,572  
PRIOR FILING DATE: 2004-05-14  
PRIOR APPLICATION NUMBER: US 60/666,340  
PRIOR FILING DATE: 2005-03-30  
PRIOR APPLICATION NUMBER: US 60/665,094  
PRIOR FILING DATE: 2005-03-25  
PRIOR APPLICATION NUMBER: US 60/662,742  
PRIOR FILING DATE: 2005-03-17  
PRIOR APPLICATION NUMBER: US 60/593,329  
PRIOR FILING DATE: 2005-01-06  
PRIOR APPLICATION NUMBER: US 60/593,081  
PRIOR FILING DATE: 2004-12-08  
PRIOR APPLICATION NUMBER: US 60/522,860  
PRIOR FILING DATE: 2004-11-15  
PRIOR APPLICATION NUMBER: US 60/522,457  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 760616  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 520800  
LENGTH: 64  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-130-645A-520800

Query Match 23.8%; Score 20.2; DB 19; Length 64;  
Best Local Similarity 59.6%; Pred. No. 4.7e+03;  
Matches 34; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 12 AACUGAGAGGGCGUGGUUAGCGGCCCAAGUUGAAGGGCGCUUUCUGUUU 68  
|||||  
Db 1 AAAGAAGAGGGCCAGCUUAGGUGUUGACUGUUGAAGGAGUAGAAUUCUGUCU 57

RESULT 15  
US-11-130-645A-618491  
Sequence 618491, Application US/11130645A

```

; Publication No. US20070050146A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Amir, Avniel
; APPLICANT: Yael, Karov
; APPLICANT: Ranit, Aharonov
; TITLE OF INVENTION: MicroRNAs and Uses Thereof
; FILE REFERENCE: 06087.0202.CPUS13
; CURRENT APPLICATION NUMBER: US/11/130.645A
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: PCT/US05/16986
; PRIOR FILING DATE: 2005-05-14
; PRIOR APPLICATION NUMBER: US 10/709,577
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 10/709,572
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/666,340
; PRIOR FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: US 60/665,094
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/662,742
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US 60/593,329
; PRIOR FILING DATE: 2005-01-06
; PRIOR APPLICATION NUMBER: US 60/593,081
; PRIOR FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: US 60/522,860
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/522,457
; PRIOR FILING DATE: 2004-10-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 618491
; LENGTH: 64
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-130-645A-618491

```

```

Query Match      23.8%; Score 20.2; DB 19; Length 64;
Best Local Similarity 75.8%; Pred. NO. 4.7e+03;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

```

QY      42 AGUUGGAAGCGCGUUGCUUGUUGUUGUUGUUGA 74
DB      7 AUUGGAUAGGAUUGGUCUUGUUGUUGUUGA 39

```

Search completed: June 19, 2007, 18:08:19  
Job time : 1268 secs

GENCORE VERSION 8.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

3  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400  
401  
402  
403  
404  
405  
406  
407  
408  
409  
410  
411  
412  
413  
414  
415  
416  
417  
418  
419  
420  
421  
422  
423  
424  
425  
426  
427  
428  
429  
430  
431  
432  
433  
434  
435  
436  
437  
438  
439  
440  
441  
442  
443  
444  
445  
446  
447  
448  
449  
450  
451  
452  
453  
454  
455  
456  
457  
458  
459  
460  
461  
462  
463  
464  
465  
466  
467  
468  
469  
470  
471  
472  
473  
474  
475  
476  
477  
478  
479  
480  
481  
482  
483  
484  
485  
486  
487  
488  
489  
490  
491  
492  
493  
494  
495  
496  
497  
498  
499  
500  
501  
502  
503  
504  
505  
506  
507  
508  
509  
510  
511  
512  
513  
514  
515  
516  
517  
518  
519  
520  
521  
522  
523  
524  
525  
526  
527  
528  
529  
530  
531  
532  
533  
534  
535  
536  
537  
538  
539  
540  
541  
542  
543  
544  
545  
546  
547  
548  
549  
550  
551  
552  
553  
554  
555  
556  
557  
558  
559  
560  
561  
562  
563  
564  
565  
566  
567  
568  
569  
570  
571  
572  
573  
574  
575  
576  
577  
578  
579  
580  
581  
582  
583  
584  
585  
586  
587  
588  
589  
590  
591  
592  
593  
594  
595  
596  
597  
598  
599  
600  
601  
602  
603  
604  
605  
606  
607  
608  
609  
610  
611  
612  
613  
614  
615  
616  
617  
618  
619  
620  
621  
622  
623  
624  
625  
626  
627  
628  
629  
630  
631  
632  
633  
634  
635  
636  
637  
638  
639  
640  
641  
642  
643  
644  
645  
646  
647  
648  
649  
650  
651  
652  
653  
654  
655  
656  
657  
658  
659  
660  
661  
662  
663  
664  
665  
666  
667  
668  
669  
670  
671  
672  
673  
674  
675  
676  
677  
678  
679  
680  
681  
682  
683  
684  
685  
686  
687  
688  
689  
690  
691  
692  
693  
694  
695  
696  
697  
698  
699  
700  
701  
702  
703  
704  
705  
706  
707  
708  
709  
710  
711  
712  
713  
714  
715  
716  
717  
718  
719  
720  
721  
722  
723  
724  
725  
726  
727  
728  
729  
730  
731  
732  
733  
734  
735  
736  
737  
738  
739  
740  
741  
742  
743  
744  
745  
746  
747  
748  
749  
750  
751  
752  
753  
754  
755  
756  
757  
758  
759  
760  
761  
762  
763  
764  
765  
766  
767  
768  
769  
770  
771  
772  
773  
774  
775  
776  
777  
778  
779  
780  
781  
782  
783  
784  
785  
786  
787  
788  
789  
790  
791  
792  
793  
794  
795  
796  
797  
798  
799  
800  
801  
802  
803  
804  
805  
806  
807  
808  
809  
810  
811  
812  
813  
814  
815  
816  
817  
818  
819  
820  
821  
822  
823  
824  
825  
826  
827  
828  
829  
830  
831  
832  
833  
834  
835  
836  
837  
838  
839  
840  
841

```

Query Match      25.6%; Score 21.8; DB 11; Length 81;
Best Local Similarity 40.8%; Pred. No. 2.3e+04;
Matches 20; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY      23  GCUGGUUAAGGCGUCGCCCAAGTUGAAGGCGCGCUCUGUCUGUUCU 71
Dh      3  GTGGATTGTCGGGACACAGATTGTCGCGCTCATTTCCAACTCCCTCT 51

```



```

RESULT 3
DY796917      73 bp      mRNA      linear      EST 21-MAR-2006
PMAL-aa57b05.b1 Lamprey_EST_Tissues Petromyzon marinus.cDNA 3',
mRNA sequence.
DY796917
DY796917.1   GI:90141134
EST.
Petromyzon marinus (sea lamprey)
Petromyzon marinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
1 (bases 1 to 73)
Wilson,R.
WashU Lamprey EST project
Unpublished (2005)
Contact: Ziping Zhang
WashU Lamprey EST project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: submissions@watson.wustl.edu
Library material provided by Department of Fisheries & Wildlife,
Michigan State University Library constructed by Ziping Zhang;
Yilei Wang; Weiming Li Library sequenced by Washington University
Genome Sequencing Center
This trace has been recalled with phred
original value before phred recall for SL was 0
original value before phred recall for SR was 122
Seq primer: PDNR-LIB-reverse.
Location/Qualifiers
1..73
/organism="Petromyzon marinus"
/mol_type="mRNA"
/db_xref="taxon:7757"
/sex="Mlx"
/dev_stage="Adult"
/lab_host="DH10B"
/clone_lib="Lamprey EST Tissues"
/note="Vector: pDNR-LIB; Site_1: Sfi I; Site_2: Sfi I"

FEATURES
source
Query Match      24.7%; Score 21; DB 12; Length 73;
Best Local Similarity 40.5%; Pred.No. 4.2e+04;
Matches 15; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 49 AGGCGCGUUGCUUGUUUUGGAGUGCAGAGUCCU 85
||||| :::: :::: :::: :::: :::: :::: ::::
DB 21 AGCGTTTTTTTTTTTTTTTTTTGGTGATTCAGAGCCCT 57

RESULT 4
AV858990/c
LOCUS
DEFINITION
AV858990 Nori Satoh unpublished cDNA library, larva Ciona
intestinalis cDNA clone rcilv21o13 3', mRNA sequence.
ACCESSION
AV858990
VERSION
AV858990.1 GI:16846514
KEYWORDS
EST.
SOURCE
Ciona intestinalis
ORGANISM
Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 77)
Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
Expressed genes in Ciona intestinalis
Unpublished (2000)
Contact: Nori Satoh
Department of Zoology
Kyoto University

```



[illegible]

```

/dev_stage="2-cell"
/lab_host="DH10B"
/clone_lib="Knowles Solter mouse 2 cell"
/note="Organ: embryo. Vector: Bluescribe (modified)."

```

ACCESSION  
VERSION  
KEYWORD



TDNA. This sequence lies within an annotated exon of At5g65210.

Class: TDNA tagged.

Location/Qualifiers

# FEATURES

source

1..65  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /ecotype="Col-0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_028210.16.80.n"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

## ORIGIN

Query Match 22.4%; Score 19; DB 16; Length 65;  
 Best Local Similarity 50.0%; Pred. No. 1.9e+05;  
 Matches 18; Conservative 7; Mismatches 11; Indels 0; Gaps 0;  
 QY 4 UUAUCUGCAACUGAGAGCGGCGUGUUAAGCGGCCCC 39  
 Db 48 TTNTGTGCCACCGAGAGAGTTGGTATATGCGTACC 13

Search completed: June 19, 2007, 17:47:05  
 Job time : 4746 secs

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 12:41:00 ; Search time 1106 Seconds  
(without alignments)  
1499,898 Million cell updates/sec

Title: US-10-604-726A-6034  
Perfect score: 24  
Sequence: 1 ugagagggcugguuaagcgucc 24

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 2038054

Minimum DB seq length: 0  
Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*  
1: gb\_env.\*  
2: gb\_pat.\*  
3: gb\_ph.\*  
4: gb\_pl.\*  
5: gb\_pr.\*  
6: gb\_ro.\*  
7: gb\_sts.\*  
8: gb\_sy.\*  
9: gb\_un.\*  
10: gb\_vi.\*  
11: gb\_ov.\*  
12: gb\_htg.\*  
13: gb\_in.\*  
14: gb\_om.\*  
15: gb\_ba.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	15.8	65.8	24	2	AX443910 Sequence
2	15.8	65.8	25	2	AX447886 Sequence
C 3	14.6	60.8	24	2	DD122759 NUCLEAR H
C 4	14.6	60.8	24	2	AX538707 Sequence
C 5	14.4	60.0	21	2	BD353840 Method of
C 6	13.8	57.5	22	2	AR036420 Sequence
C 7	13.8	57.5	22	2	I29861 Sequence 12
C 8	13.2	55.0	25	2	AR148541 Sequence
C 9	13.2	55.0	25	2	I62320 Sequence 23
C 10	13	54.2	17	2	BD379515 Method an
C 11	13	54.2	17	2	BD379516 Method an
C 12	13	54.2	17	2	BD379517 Method an
C 13	13	54.2	17	2	BD379518 Method an
C 14	13	54.2	17	2	AX215297 Sequence
C 15	13	54.2	17	2	AX215298 Sequence
C 16	13	54.2	17	2	AX215299 Sequence
C 17	13	54.2	17	2	AX215300 Sequence
C 18	13	54.2	20	2	BD405918 GENE AND

C 19	13	54.2	20	2	AX298773 Sequence
C 20	12.8	53.3	19	2	AR069252 Sequence
C 21	12.8	53.3	19	2	CS101953 Sequence
C 22	12.8	53.3	19	2	CS102090 Sequence
C 23	12.8	53.3	24	6	DQ755439 Rattus no
C 24	12.8	53.3	25	2	AR240243 Sequence
C 25	12.6	52.5	19	2	AR628705 Sequence
C 26	12.6	52.5	20	2	AR100388 Sequence
C 27	12.6	52.5	20	2	AR150043 Sequence
C 28	12.6	52.5	20	2	BD227916 Antisense
C 29	12.6	52.5	20	2	BD278694 Oligonucle
C 30	12.6	52.5	20	2	AR442443 Sequence
C 31	12.6	52.5	20	8	AB213914 Synthetic
C 32	12.6	52.5	21	2	AR231257 Sequence
C 33	12.6	52.5	22	2	BD301800 Pollinosi
C 34	12.6	52.5	22	2	CS020856 Sequence
C 35	12.6	52.5	25	2	AR404657 Sequence
C 36	12.4	51.7	20	2	BD272896 Control o
C 37	12.4	51.7	20	2	DD136913 A Pharmac
C 38	12.4	51.7	21	2	DD271504 Methods t
C 39	12.4	51.7	21	2	DD271505 Methods t
C 40	12.4	51.7	21	2	DD271506 Methods t
C 41	12.4	51.7	22	2	DD027364 Synthetic
C 42	12.4	51.7	24	2	AR151401 Sequence
C 43	12.4	51.7	24	2	CQ816772 Sequence
C 44	12.4	51.7	24	2	AX443802 Sequence
C 45	12.4	51.7	25	2	AX447783 Sequence

ALIGNMENTS

RESULT 1	AX443910	AX443910	24 bp	DNA	linear	PAT 03-JUL-2002
LOCUS	Sequence 365 from Patent WO0216649.					
DEFINITION	AX443910					
ACCESSION	AX443910.1	GI:21691188				
VERSION						
KEYWORDS	synthetic construct					
SOURCE	synthetic construct					
ORGANISM	other sequences; artificial sequences.					
REFERENCE	1					
AUTHORS	Gunderson,K.					
TITLE	Probes and decoder oligonucleotides					
JOURNAL	Patent: WO 0216649-A 365 28-FEB-2002;					
ILLUMINA, INC. (US)						
FEATURES	Location/Qualifiers					
source	1..24					
	/organism="synthetic construct"					
	/mol_type="unassigned DNA"					
	/db_xref="taxon:32630"					
	/note="Computer Generated Probe Sequence."					

ORIGIN	Query Match	65.8%;	Score 15.8;	DB 2;	Length 24;	
	Best Local Similarity	73.7%;	Pred. No. 6.8e+04;			
	Matches 14;	Conservative 3;	Mismatches 2;	Indels 0;	Gaps 0;	
QY	2	GAGAGGGCGUGGUUAGGC 20				
Db	4	GAGAGGGCGTTGGTTAAGGC 22				
RESULT 2	AX447886	AX447886	25 bp	DNA	linear	PAT 03-JUL-2002
LOCUS	Sequence 4341 from Patent WO0216649.					
DEFINITION	AX447886					
ACCESSION	AX447886.1	GI:21696785				
VERSION						
KEYWORDS	synthetic construct					
SOURCE	synthetic construct					
ORGANISM						

```

other sequences; artificial sequences.
1
REFERENCE
AUTHORS Gunderson,K.
TITLE Probes and decoder oligonucleotides
JOURNAL Patent: WO 0216649-A 4341 28-FEB-2002;
Illumina, Inc. (US)
FEATURES
source
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Computer Generated Probe Sequence."
ORIGIN
Query Match 65.8%; Score 15.8; DB 2; Length 25;
Best Local Similarity 73.7%; Pred. No. 6.7e+04;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 2 GAGAGGGCGUGUUAAGGC 20
||||| :|||
Db 5 GAGAGGGCGTGTAAAGC 23

RESULT 3
DD122759/c 24 bp DNA linear PAT 04-NOV-2005
LOCUS DD122759 NUCLEAR HORMONE RECEPTOR LIGAND BINDING DOMAIN.
DEFINITION DD122759
ACCESSION DD122759
VERSION DD122759.1 GI:92809446
KEYWORDS JP 2005500010-A/4.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 24)
AUTHORS Pierron,V.N., Allen,J.M., Allen,K.E., Phillips,T., Phelps,C.B.,
Fagan,K.J. and Potter,S.J.
TITLE NUCLEAR HORMONE RECEPTOR LIGAND BINDING DOMAIN
JOURNAL Patent: JP 2005500010-A 4 06-JAN-2005;
INPHARMATICA LIMITED
COMMENT OS Artificial Sequence
PN JP 2005500010-A/4
PD 06-JAN-2005
PR 05-MAR-2002 JP 2002569876
PR 05-MAR-2001 GB 0105402.2
PI valerie nathalie pierron,janet marjorie allen,kathryn PI
elizabeth allen,
PI tom phillips,christopher benjamin phelps,richard joseph fagan,
PI sarah jane potter
CC LBDG3 Reverse primer
FH Key Location/Qualifiers.
FEATURES
source
1. .24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 60.8%; Score 14.6; DB 2; Length 24;
Best Local Similarity 61.9%; Pred. No. 2.5e+05;
Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
Qy 3 AGAGGGCGUGUUAAGGCUC 23
||||| :|||
Db 23 AGAGGGCGTATTAACTGTC 3

RESULT 4
AX538707/c 24 bp DNA linear PAT 23-NOV-2002
LOCUS AX538707
DEFINITION AX538707
ACCESSION AX538707
VERSION AX538707.1 GI:25271321
KEYWORDS
other sequences; artificial sequences.
1
REFERENCE
AUTHORS Fagan,R.J., Phelps,C.B., Phillips,T., Pierron,V.N., Allen,K.E.,
Allen,J.M. and Potter,S.J.
TITLE Nuclear hormone receptor ligand binding domain
JOURNAL Patent: WO 02070557-A 6 12-SEP-2002;
Inpharmatica Limited (GB)
FEATURES
source
1. .24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="LBDG3 Reverse primer"
ORIGIN
Query Match 60.8%; Score 14.6; DB 2; Length 24;
Best Local Similarity 61.9%; Pred. No. 2.5e+05;
Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
Qy 3 AGAGGGCGUGUUAAGGCUC 23
||||| :|||
Db 23 AGAGGGCGTATTAACTGTC 3

RESULT 5
BD353840/c 21 bp DNA linear PAT 04-NOV-2005
LOCUS BD353840
DEFINITION BD353840 Method of food analysis.
ACCESSION BD353840
VERSION BD353840.1 GI:92254966
KEYWORDS WO 03068964-A/7.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 21)
AUTHORS Yamakawa,H., Suzuki,E., Miyatake,K. and Hayakawa,K.
TITLE Method of food analysis
JOURNAL Patent: WO 03068964-A 7 21-AUG-2003;
H YAMAKAWA et al
COMMENT OS Artificial Sequence
PN WO 03068964-A/7
PD 21-AUG-2003
PR 26-SEP-2002 WO 2002JP009982
PR 15-FEB-2002 JP 02P 038930
PI hirohito yamakawa,eriko suzuki,kiyoko miyatake,katsuyuki PI
hayakawa
CC FAG19, designed sense primer based on 11 between 1464 and 1484
FH Key Location/Qualifiers.
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 60.0%; Score 14.4; DB 2; Length 21;
Best Local Similarity 68.8%; Pred. No. 3.2e+05;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Qy 7 GGGCGUGUUAAGCGUC 22
||||| :|||
Db 17 GGGCTGTTATGCGCT 2

RESULT 6
AR036420/c 22 bp DNA linear PAT 29-SEP-1999
LOCUS AR036420
DEFINITION AR036420 Sequence 12 from patent US 5872214.
ACCESSION AR036420
VERSION AR036420.1 GI:5953088
KEYWORDS

```



Matches	12;	Conservative	3;	Mismatches	3;	Indels	3;	Gaps	0;
QY	5	AGGGCGUGGUUAGGCGU	22						
Db	23	AGGTGCTGGTGAAGGCAT	6						
RESULT 9									
LOCUS	162320			25 bp	DNA	linear	PAT 07-OCT-1997		
DEFINITION	Sequence 23 from patent US 5658786.								
ACCESSION	162320								
VERSION	162320.1	GI:2480268							
KEYWORDS	Unknown.								
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	1 (bases 1 to 25)								
AUTHORS	Smith,K.E., Weinschank,R.L., Borden,L.A. and Hartig,P.R.								
TITLE	DNA encoding rat taurine transporter and uses thereof								
JOURNAL	Patent: US 5658786-A 23 19-AUG-1997;								
FEATURES	Location/Qualifiers								
source	1..25								
	/organism="unknown"								
	/mol_type="unassigned DNA"								
ORIGIN									
Query Match	55.0%;	Score 13.2;	DB 2;	Length 25;					
Best Local Similarity	66.7%;	Pred. No. 1.1e+06;							
Matches	12;	Conservative	3;	Mismatches	3;	Indels	0;	Gaps	0;
QY	5	AGGGCGUGGUUAGGCGU	22						
Db	23	AGGTGCTGGTGAAGGCAT	6						
RESULT 10									
LOCUS	BD379515/c			17 bp	RNA	linear	PAT 04-NOV-2005		
DEFINITION	Method and Reagent for the Modulation and Diagnosis of CD20 and								
ACCESSION	BD379515								
VERSION	BD379515.1	GI:92278608							
KEYWORDS	JP 2003525037-A/739.								
SOURCE	synthetic construct								
ORGANISM	synthetic construct								
	other sequences; artificial sequences.								
REFERENCE	1 (bases 1 to 17)								
AUTHORS	Blatt,L., Mcswiggen,J., Chorlila,B.M. and Harbelli,P.								
TITLE	Method and Reagent for the Modulation and Diagnosis of CD20 and								
JOURNAL	NOGO Gene Expression								
COMMENT	Patent: JP 2003525037-A 739 26-AUG-2003;								
	Ribozyme Pharmaceuticals Inc								
	OS Artificial Sequence								
	PN JP 2003525037-A/739								
	PD 26-AUG-2003								
	PF 09-FEB-2001 JP 2001558241								
	PR 11-FEB-2000 US 60/181797,28-FEB-2000 US 60/185516, PR								
	06-MAR-2000 US 60/187128								
	PI lawrence blatt,james mcswiggen,blatto m chorlila,peter PI								
	harbell								
	CC Description of Artificial Sequence: Nucleic Acid FH Key								
	Location/Qualifiers.								
FEATURES	Location/Qualifiers								
source	1..17								
	/organism="synthetic construct"								
	/mol_type="unassigned RNA"								
	/db_xref="taxon:32630"								
ORIGIN									
Query Match	54.2%;	Score 13;	DB 2;	Length 17;					
Best Local Similarity	84.6%;	Pred. No. 1.5e+06;							
Matches	11;	Conservative	2;	Mismatches	0;	Indels	0;	Gaps	0;

```

Qy 1 UGAGAGGGGCTGG 13
Db 16 TGAGAGGGGCTGG 4

RESULT 11
BD379516/c
LOCUS
DEFINITION Method and Reagent for the Modulation and Diagnosis of CD20 and
ACCESSION BD379516 17 bp RNA linear PAT 04-NOV-2005
VERSION BD379516.1 GI:92278609
KEYWORDS JP 2003525037-A/740.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Mcswiggen,J., Chorlila,B.M. and Harbelle,P.
TITLE Method and Reagent for the Modulation and Diagnosis of CD20 and
JOURNAL NOGO Gene Expression
COMMENT Patent: JP 2003525037-A 740 26-AUG-2003;
Ribozyme Pharmaceuticals Inc
OS Artificial Sequence
PN JP 2003525037-A/740
PD 26-AUG-2003
PF 09-FEB-2001 JP 2001558241
PI 11-FEB-2000 US 60/181797,28-FEB-2000 US 60/185516, PR
06-MAR-2000 US 60/187128
PI Lawrence blatt,james mcswiggen,balatto m chorlila,peter PI
harbelle
CC Description of Artificial Sequence: Nucleic Acid FH Key
Location/Qualifiers
FEATURES
source
1..17
/mol_type="synthetic construct"
/db_xref="taxon:32630"
ORIGIN
Query Match 54.2%; Score 13; DB 2; Length 17;
Best Local Similarity 84.6%; Pred. No. 1.5e+06;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 UGAGAGGGGCTGG 13
Db 14 TGAGAGGGGCTGG 2

RESULT 12
BD379517/c
LOCUS
DEFINITION Method and Reagent for the Modulation and Diagnosis of CD20 and
ACCESSION BD379517 17 bp RNA linear PAT 04-NOV-2005
VERSION BD379517.1 GI:92278610
KEYWORDS JP 2003525037-A/741.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Mcswiggen,J., Chorlila,B.M. and Harbelle,P.
TITLE Method and Reagent for the Modulation and Diagnosis of CD20 and
JOURNAL NOGO Gene Expression
COMMENT Patent: JP 2003525037-A 741 26-AUG-2003;
Ribozyme Pharmaceuticals Inc
OS Artificial Sequence
PN JP 2003525037-A/741
PD 26-AUG-2003
PF 09-FEB-2001 JP 2001558241
PI 11-FEB-2000 US 60/181797,28-FEB-2000 US 60/185516, PR
06-MAR-2000 US 60/187128
PI Lawrence blatt,james mcswiggen,balatto m chorlila,peter PI
harbelle
CC Description of Artificial Sequence: Nucleic Acid FH Key
Location/Qualifiers
FEATURES
source
1..17
/mol_type="synthetic construct"
/db_xref="taxon:32630"
ORIGIN
Query Match 54.2%; Score 13; DB 2; Length 17;
Best Local Similarity 84.6%; Pred. No. 1.5e+06;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 UGAGAGGGGCTGG 13
Db 15 TGAGAGGGGCTGG 3

RESULT 13
BD379518/c
LOCUS
DEFINITION Method and Reagent for the Modulation and Diagnosis of CD20 and
ACCESSION BD379518 17 bp RNA linear PAT 04-NOV-2005
VERSION BD379518.1 GI:92278611
KEYWORDS JP 2003525037-A/742.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Mcswiggen,J., Chorlila,B.M. and Harbelle,P.
TITLE Method and Reagent for the Modulation and Diagnosis of CD20 and
JOURNAL NOGO Gene Expression
COMMENT Patent: JP 2003525037-A 742 26-AUG-2003;
Ribozyme Pharmaceuticals Inc
OS Artificial Sequence
PN JP 2003525037-A/742
PD 26-AUG-2003
PF 09-FEB-2001 JP 2001558241
PI 11-FEB-2000 US 60/181797,28-FEB-2000 US 60/185516, PR
06-MAR-2000 US 60/187128
PI Lawrence blatt,james mcswiggen,balatto m chorlila,peter PI
harbelle
CC Description of Artificial Sequence: Nucleic Acid FH Key
Location/Qualifiers
FEATURES
source
1..17
/mol_type="synthetic construct"
/db_xref="taxon:32630"
ORIGIN
Query Match 54.2%; Score 13; DB 2; Length 17;
Best Local Similarity 84.6%; Pred. No. 1.5e+06;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 UGAGAGGGGCTGG 13
Db 13 TGAGAGGGGCTGG 1

RESULT 14
AX215297/c
LOCUS
DEFINITION Sequence 739 from Patent WO0159103.
ACCESSION AX215297 17 bp RNA linear PAT 07-SEP-2001
VERSION AX215297.1 GI:15525340
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1

```

AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and  
nogo gene expression  
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
McSwiggen, James (US) ; Chowrira, Bharat M. (US)

FEATURES  
source 1. .17  
Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"

## ORIGIN

Query Match 54.2%; Score 13; DB 2; Length 17;  
Best Local Similarity 84.6%; Pred. No. 1.5e+06;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGAGAGGGGCGG 13  
:|||||:|  
Db 16 TGAGAGGGGCTGG 4

## RESULT 15

AX215298/c  
LOCUS AX215298 17 bp RNA linear PAT 07-SEP-2001  
DEFINITION Sequence 740 from Patent WO0159103.  
ACCESSION AX215298  
VERSION AX215298.1 GI:15525341  
KEYWORDS  
synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

## REFERENCE 1

AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and  
nogo gene expression  
JOURNAL Patent: WO 0159103-A 740 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
McSwiggen, James (US) ; Chowrira, Bharat M. (US)

FEATURES  
source 1. .17  
Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"

## ORIGIN

Query Match 54.2%; Score 13; DB 2; Length 17;  
Best Local Similarity 84.6%; Pred. No. 1.5e+06;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGAGAGGGGCGG 13  
:|||||:|  
Db 15 TGAGAGGGGCTGG 3

Search completed: June 19, 2007, 13:51:02  
Job time : 1109 secs

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 12:28:50 ; Search time 246 Seconds  
(without alignments)  
721.516 Million cell updates/sec

Title: US-10-604-726A-6034  
Perfect score: 24  
Sequence: 1 ugagagggcgguaagcgucc 24

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 4355164

Minimum DB seq length: 0  
Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq\_200701.\*  
1: geneseqn1980s.\*  
2: geneseqn1990s.\*  
3: geneseqn2000s.\*  
4: geneseqn2001as.\*  
5: geneseqn2001bs.\*  
6: geneseqn2002as.\*  
7: geneseqn2002bs.\*  
8: geneseqn2003as.\*  
9: geneseqn2003bs.\*  
10: geneseqn2003cs.\*  
11: geneseqn2003ds.\*  
12: geneseqn2004as.\*  
13: geneseqn2004bs.\*  
14: geneseqn2005s.\*  
15: geneseqn2006s.\*  
16: geneseqn2007s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.8	65.8	24	6	ABQ11002
2	15.8	65.8	24	6	ABQ04674
3	15.8	65.8	24	6	ABQ04715
4	15.8	65.8	24	6	ABQ00358
5	15.8	65.8	24	6	ABQ11043
6	15.8	65.8	25	6	ABQ12538
7	15.8	65.8	25	6	ABQ12579
8	14.6	60.8	24	6	AAL50117
9	14.4	60.0	21	9	ADA24254
10	14.2	59.2	20	14	ADZ97885
11	14.2	59.2	21	11	ADJ13347
12	14.2	59.2	25	3	AAA61591
13	14	58.3	25	9	ACI82777
14	13.8	57.5	17	8	ACD57816
15	13.8	57.5	17	12	ADI83268
16	13.8	57.5	22	2	AAT47817
17	13.8	57.5	22	2	AAX04299

18	13.6	56.7	21	14	ACL41634
19	13.6	56.7	21	14	ACL41632
20	13.6	56.7	21	14	ACL43064
21	13.6	56.7	23	15	AEJ80377
22	13.2	55.0	19	14	AEA25301
23	13.2	55.0	19	14	AEA25458
24	13.2	55.0	20	10	ABZ99113
25	13.2	55.0	20	11	ABD32144
26	13.2	55.0	20	12	ADJ60998
27	13.2	55.0	20	12	ADO46487
28	13.2	55.0	20	14	ADZ97886
29	13.2	55.0	20	14	AED42052
30	13.2	55.0	21	11	ADJ13385
31	13.2	55.0	21	13	ADU43508
32	13.2	55.0	25	5	AAP85432
33	13.2	55.0	25	9	ACK10389
34	13.2	55.0	25	10	AAD64634
35	13.2	55.0	25	12	ADO61007
36	13.2	55.0	25	14	AEC90171
37	13	54.2	17	4	ABK00741
38	13	54.2	17	4	ABK00742
39	13	54.2	17	4	ABK00739
40	13	54.2	17	4	ABK00740
41	13	54.2	20	6	AS97797
42	13	54.2	20	12	ADM16137
43	13	54.2	21	14	ACL43063
44	13	54.2	21	14	ACL42274
45	13	54.2	25	9	ACI36340

## ALIGNMENTS

RESULT 1  
ABQ11002  
ID ABQ11002 standard; DNA; 24 BP.

XX AC ABQ11002;  
XX 11-JUN-2002 (first entry)  
XX DE Oligonucleotide adapter/capture probe 10993.  
XX KW Oligonucleotide array; adapter sequence; probe; ss.  
XX OS Synthetic.  
XX PN WO200216649-A2.  
XX PD 28-FEB-2002.  
XX PP 27-AUG-2001; 2001WO-US026519.  
XX PR 25-AUG-2000; 2000US-0227948P.  
XX PR 29-AUG-2000; 2000US-0228854P.  
XX (ILLU-) ILLUMINA INC.  
XX Gunderson K;  
XX WPI; 2002-292068/33.

Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising different specific capture probes.  
Claim 1; Page 225; 261pp; English.

The invention relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-10.

CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid  
CC and contacting the modified target nucleic acid with (I). The steps of  
CC above method is useful for detecting a target nucleic acid, which further  
CC comprises detecting the presence of the modified target nucleic acid

XX SQ Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 65.8%; Score 15.8; DB 6; Length 24;  
Best Local Similarity 73.7%; Pred. No. 1.4e+03;  
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGAGGGCGUGGUAAGGC 20  
||||| :||:|||||  
Db 4 GAGAGGGCGTGGTTAAGGC 22

RESULT 2  
ABQ04674  
ID ABQ04674 standard; DNA; 24 BP.

XX AC ABQ04674;

XX DT 11-JUN-2002 (first entry)

XX DE Oligonucleotide adapter/capture probe 4665.

XX KW Oligonucleotide array; adapter sequence; probe; ss.

XX OS Synthetic.

XX PN WO200216649-A2.

XX PD 28-FEB-2002.

XX PF 27-AUG-2001; 2001WO-US026519.

XX PR 25-AUG-2000; 2000US-0227948P.

XX PR 29-AUG-2000; 2000US-0228854P.

XX FA (ILLU-) ILLUMINA INC.

XX XX Gunderson K;

XX PI WPI; 2002-292068/33.

XX Array comprising adapter sequences useful for immobilizing or detecting a  
PT target nucleic acid sequence, has different addresses comprising  
PT different specific capture probes.

XX PS Claim 1; Page 147; 261pp; English.

XX CC The invention relates to an oligonucleotide array (I) comprising at least  
CC 25 different addresses (adapter sequences) with each comprising a  
CC different capture probe selected from a group consisting of the sequences  
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target  
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-  
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid  
CC and contacting the modified target nucleic acid with (I). The steps of  
CC above method is useful for detecting a target nucleic acid, which further  
CC comprises detecting the presence of the modified target nucleic acid

XX SQ Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 65.8%; Score 15.8; DB 6; Length 24;  
Best Local Similarity 73.7%; Pred. No. 1.4e+03;  
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGAGGGCGUGGUAAGGC 20

Db 4 GAGAGGGCGTGGTTAAGGC 22

RESULT 3

ABQ04715/c  
ID ABQ04715 standard; DNA; 24 BP.

XX AC ABQ04715;

XX DT 11-JUN-2002 (first entry)

XX DE Oligonucleotide adapter/capture probe 4706.

XX KW Oligonucleotide array; adapter sequence; probe; ss.

XX OS Synthetic.

XX PN WO200216649-A2.

XX PD 28-FEB-2002.

XX PF 27-AUG-2001; 2001WO-US026519.

XX PR 25-AUG-2000; 2000US-0227948P.

XX PR 29-AUG-2000; 2000US-0228854P.

XX PA (ILLU-) ILLUMINA INC.

XX PI Gunderson K;

XX DR WPI; 2002-292068/33.

XX Array comprising adapter sequences useful for immobilizing or detecting a  
PT target nucleic acid sequence, has different addresses comprising  
PT different specific capture probes.

XX PS Claim 1; Page 147; 261pp; English.

XX CC The invention relates to an oligonucleotide array (I) comprising at least  
CC 25 different addresses (adapter sequences) with each comprising a  
CC different capture probe selected from a group consisting of the sequences  
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target  
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-  
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid  
CC and contacting the modified target nucleic acid with (I). The steps of  
CC above method is useful for detecting a target nucleic acid, which further  
CC comprises detecting the presence of the modified target nucleic acid

XX SQ Sequence 24 BP; 5 A; 10 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 65.8%; Score 15.8; DB 6; Length 24;

Best Local Similarity 73.7%; Pred. No. 1.4e+03;

Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGAGGGCGUGGUAAGGC 20

Db 21 GAGAGGGCGTGGTTAAGGC 3

RESULT 4

ABQ00358

ID ABQ00358 standard; DNA; 24 BP.

XX AC ABQ00358;

XX DT 11-JUN-2002 (first entry)

XX DE Oligonucleotide adapter/capture probe 349.

XX KW Oligonucleotide array; adapter sequence; probe; ss.

XX OS Synthetic.

XX PN WO200216649-A2.

XX PD 28-FEB-2002.

CC	The invention relates to an oligonucleotide array (I) comprising at least	
CC	25 different addresses (adapter sequences) with each comprising a	
CC	different capture probe selected from a group consisting of the sequences	
CC	given in ABQ00010-ABQ13409. (I) is useful for immobilising a target	
CC	nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-	
CC	ABQ13409) to a target nucleic acid to form a modified target nucleic acid	
CC	and contacting the modified target nucleic acid with (I). The steps of	
CC	above method is useful for detecting a target nucleic acid, which further	
CC	comprises detecting the presence of the modified target nucleic acid	
XX		
SQ	Sequence 24 BP; 5 A; 10 C; 2 G; 7 T; 0 U; 0 Other;	
	Query Match 55.8%; Score 15.8; DB 6; Length 24;	
	Best Local Similarity 73.7%; Pred. No. 1.4e+03;	
	Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0	
QY	2 GAGAGGGCGUGGUUAGGC 20	
DB	21 GAGAGGGCGTGGTTAAGGC 3	
	:	
RESULT 6		
ABQ12538		
ID	ABQ12538 standard; DNA; 25 BP.	
XX	AC AC	
XX	ABQ12538;	
DT	11-JUN-2002 (first entry)	
XX		
DE	Oligonucleotide adapter/capture probe 12529.	
XX		
KW	Oligonucleotide array; adapter sequence; probe; ss.	
OS	Synthetic.	
XX		
PN	WO200216649-A2.	
XX		
PD	28-FEB-2002.	
XX		
PF	27-AUG-2001; 2001WO-US026519.	
XX		
PR	25-AUG-2000; 2000US-0227948P.	
PR	29-AUG-2000; 2000US-0228854P.	
XX		
PA	(ILLU-) ILLUMINA INC.	
XX		
PI	Gunderson K;	
XX		
DR	WPI; 2002-292068/33.	
XX		
PT	Array comprising adapter sequences useful for immobilizing or detecting a	
PT	target nucleic acid sequence, has different addresses comprising	
PT	different specific capture probes.	
XX		
XX	Claim 1; Page 244; 261pp; English.	
PS		
XX		
CC	The invention relates to an oligonucleotide array (I) comprising at least	
CC	25 different addresses (adapter sequences) with each comprising a	
CC	different capture probe selected from a group consisting of the sequences	
CC	given in ABQ00010-ABQ13409. (I) is useful for immobilising a target	
CC	nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-	
CC	ABQ13409) to a target nucleic acid to form a modified target nucleic acid	
CC	and contacting the modified target nucleic acid with (I). The steps of	
CC	above method is useful for detecting a target nucleic acid, which further	
CC	comprises detecting the presence of the modified target nucleic acid	
XX		
SQ	Sequence 25 BP; 7 A; 2 C; 10 G; 6 T; 0 U; 0 Other;	
	Query Match 65.8%; Score 15.8; DB 6; Length 25;	
	Best Local Similarity 73.7%; Pred. No. 1.4e+03;	
	Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0	
QY	2 GAGAGGGCGUGGUUAGGC 20	

KW cancer; autoimmune disorder; HIV; neurological; dermatological; anti-HIV; neuro

KW cancer; autoimmune disorder; inflammation; FCR; antiseptolitic;  
KW dermatological; anti-HIV; neuroprotective; nephrotropic; antianginal;  
KW

XX  
1907-1908  
(continued)  
1908-1909  
1909-1910  
1910-1911  
1911-1912  
1912-1913  
1913-1914  
1914-1915  
1915-1916  
1916-1917  
1917-1918  
1918-1919  
1919-1920  
1920-1921  
1921-1922  
1922-1923  
1923-1924  
1924-1925  
1925-1926  
1926-1927  
1927-1928  
1928-1929  
1929-1930  
1930-1931  
1931-1932  
1932-1933  
1933-1934  
1934-1935  
1935-1936  
1936-1937  
1937-1938  
1938-1939  
1939-1940  
1940-1941  
1941-1942  
1942-1943  
1943-1944  
1944-1945  
1945-1946  
1946-1947  
1947-1948  
1948-1949  
1949-1950  
1950-1951  
1951-1952  
1952-1953  
1953-1954  
1954-1955  
1955-1956  
1956-1957  
1957-1958  
1958-1959  
1959-1960  
1960-1961  
1961-1962  
1962-1963  
1963-1964  
1964-1965  
1965-1966  
1966-1967  
1967-1968  
1968-1969  
1969-1970  
1970-1971  
1971-1972  
1972-1973  
1973-1974  
1974-1975  
1975-1976  
1976-1977  
1977-1978  
1978-1979  
1979-1980  
1980-1981  
1981-1982  
1982-1983  
1983-1984  
1984-1985  
1985-1986  
1986-1987  
1987-1988  
1988-1989  
1989-1990  
1990-1991  
1991-1992  
1992-1993  
1993-1994  
1994-1995  
1995-1996  
1996-1997  
1997-1998  
1998-1999  
1999-2000  
2000-2001  
2001-2002  
2002-2003  
2003-2004  
2004-2005  
2005-2006  
2006-2007  
2007-2008  
2008-2009  
2009-2010  
2010-2011  
2011-2012  
2012-2013  
2013-2014  
2014-2015  
2015-2016  
2016-2017  
2017-2018  
2018-2019  
2019-2020  
2020-2021  
2021-2022  
2022-2023  
2023-2024  
2024-2025  
2025-2026  
2026-2027  
2027-2028  
2028-2029  
2029-2030  
2030-2031  
2031-2032  
2032-2033  
2033-2034  
2034-2035  
2035-2036  
2036-2037  
2037-2038  
2038-2039  
2039-2040  
2040-2041  
2041-2042  
2042-2043  
2043-2044  
2044-2045  
2045-2046  
2046-2047  
2047-2048  
2048-2049  
2049-2050  
2050-2051  
2051-2052  
2052-2053  
2053-2054  
2054-2055  
2055-2056  
2056-2057  
2057-2058  
2058-2059  
2059-2060  
2060-2061  
2061-2062  
2062-2063  
2063-2064  
2064-2065  
2065-2066  
2066-2067  
2067-2068  
2068-2069  
2069-2070  
2070-2071  
2071-2072  
2072-2073  
2073-2074  
2074-2075  
2075-2076  
2076-2077  
2077-2078  
2078-2079  
2079-2080  
2080-2081  
2081-2082  
2082-2083  
2083-2084  
2084-2085  
2085-2086  
2086-2087  
2087-2088  
2088-2089  
2089-2090  
2090-2091  
2091-2092  
2092-2093  
2093-2094  
2094-2095  
2095-2096  
2096-2097  
2097-2098  
2098-2099  
2099-2100  
2100-2101  
2101-2102  
2102-2103  
2103-2104  
2104-2105  
2105-2106  
2106-2107  
2107-2108  
2108-2109  
2109-2110  
2110-2111  
2111-2112  
2112-2113  
2113-2114  
2114-2115  
2115-2116  
2116-2117  
2117-2118  
2118-2119  
2119-2120  
2120-2121  
2121-2122  
2122-2123  
2123-2124  
2124-2125  
2125-2126  
2126-2127  
2127-2128  
2128-2129  
2129-2130  
2130-2131  
2131-2132  
2132-2133  
2133-2134  
2134-2135  
2135-2136  
2136-2137  
2137-2138  
2138-2139  
2139-2140  
2140-2141  
2141-2142  
2142-2143  
2143-2144  
2144-2145  
2145-2146  
2146-2147  
2147-2148  
2148-2149  
2149-2150  
2150-2151  
2151-2152  
2152-2153  
2153-2154  
2154-2155  
2155-2156  
2156-2157  
2157-2158  
2158-2159  
2159-2160  
2160-2161  
2161-2162  
2162-2163  
2163-2164  
2164-2165  
2165-2166  
2166-2167  
2167-2168  
2168-2169  
2169-2170  
2170-2171  
2171-2172  
2172-2173  
2173-2174  
2174-2175  
2175-2176  
2176-2177  
2177-2178  
2178-2179  
2179-2180  
2180-2181  
2181-2182  
2182-2183  
2183-2184  
2184-2185  
2185-2186  
2186-2187  
2187-2188  
2188-2189  
2189-2190  
2190-2191  
2191-2192  
2192-2193  
2193-2194  
2194-2195  
2195-2196  
2196-2197  
2197-2198  
2198-2199  
2199-2200  
2200-2201  
2201-2202  
2202-2203  
2203-2204  
2204-2205  
2205-2206  
2206-2207  
2207-2208  
2208-2209  
2209-2210  
2210-2211  
2211-2212  
2212-2213  
2213-2214  
2214-2215  
2215-2216  
2216-2217  
2217-2218  
2218-2219  
2219-2220  
2220-2221  
2221-2222  
2222-2223  
2223-2224  
2224-2225  
2225-2226  
2226-2227  
2227-2228  
2228-2229  
2229-2230  
2230-2231  
2231-2232  
2232-2233  
2233-2234  
2234-2235  
2235-2236  
2236-2237  
2237-2238  
2238-2239  
2239-2240  
2240-2241  
2241-2242  
2242-2243  
2243-2244  
2244-2245  
2245-2246  
2246-2247  
2247-2

111

DE Major allergenic storage protein FAGAG1 PCR primer FAG19 SEQ ID NO:7.  
XX food testing; allergen; PCR primer; Fagopyrum esculentum;  
KW major allergenic storage protein; FAGAG1; ss.  
XX Synthetic.  
OS Fagopyrum esculentum.  
XX WO2003068964-A1.  
PN 21-AUG-2003.  
XX 26-SEP-2002; 2002WO-JP009982.  
PF 15-FEB-2002; 2002JP-00038930.  
XX (NISS) NISSHIN SEIFUN GROUP INC.  
PA Yamakawa H, Suzuki E, Miyatake K, Hayakawa K;  
PI WPI; 2003-637145/60.  
XX PCR-based method for testing foods using specific primers designed from  
PT genes of target substance, useful in detecting trace components or  
PT identifying specific harmful allergens in (processed) foods.  
XX Disclosure; Page 10; 38pp; Japanese.  
XX The present invention describes a method for testing the presence or  
CC absence of a specific substance in a food by performing PCR with primers  
CC which are designed on the basis of data obtained from a part of a gene of  
CC the specific substance. Also described: (1) a similar method for  
CC detecting a trace component contained in a food, or for identifying a  
CC harmful allergen specific to a consumer of such substance by performing  
CC PCR with primers which are designed on the basis of data obtained from a  
CC part of a gene of the specific substance; (2) primers for PCR applicable  
CC in food testing which are designed on the basis of data obtained from a  
CC part of a gene of the specific substance; and (3) kits for determining  
CC concentration of a specific substance in the food containing the primers.  
CC The methods are useful for testing foods, which can be used in detecting  
CC trace components or identifying specific harmful allergens in (processed)  
CC foods, particularly applicable in food safety and management. The present  
CC sequence represents a PCR primer for a Fagopyrum esculentum major  
CC allergenic storage protein designated FAGAG1, which is used in the  
CC exemplification of the present invention.  
XX Sequence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 U; 0 Other;  
SQ Query Match 60.0%; Score 14.4; DB 9; Length 21;  
Best Local Similarity 68.8%; Pred. No. 6.2e+03;  
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
QY 7 GGGGUGUUUAGGCGU 22  
DB 17 GGGCTGGTTATGCGT 2  
RESULT 10  
ADZ97885/c  
ID ADZ97885 standard; DNA; 20 BP.  
XX AC ADZ97885;  
XX 28-JUL-2005 (first entry)  
DT Human antisense oligonucleotide SEQ ID NO:39.  
XX protein interaction; antisense oligonucleotide; ss.  
XX Homo sapiens.  
OS US2005112118-A1.  
PN Human DNA probe used to immobilise CpG methylated DNA seqid 474.  
XX

PD 26-MAY-2005.  
XX 20-OCT-2003; 2003US-00690276.  
PF 02-DEC-1999; 99US-0168377P.  
XX 02-DEC-1999; 99US-0168379P.  
PR 25-FEB-2000; 2000US-0185056P.  
PR 01-DEC-2000; 2000US-00727384.  
PR 14-DEC-2000; 2000US-0255063P.  
PR 21-DEC-2000; 2000US-0256986P.  
PR 04-JAN-2001; 2001US-0259571P.  
PR 04-JAN-2001; 2001US-0259572P.  
PR 15-MAR-2001; 2001US-0276179P.  
PR 19-MAR-2001; 2001US-0277013P.  
PR 23-JUL-2001; 2001US-0307233P.  
PR 14-DEC-2001; 2001US-00014814.  
PR 21-DEC-2001; 2001US-00024599.  
PR 04-JAN-2002; 2002US-00035343.  
PR 04-JAN-2002; 2002US-00035344.  
PR 14-MAR-2002; 2002US-00099924.  
PR 18-MAR-2002; 2002US-00100503.  
XX (MYRI-) MYRIAD GENETICS INC.  
PA Cimbara D, Heichman K, Bartel P, Mauck K, Bush A;  
PI WPI; 2005-371623/38.  
XX Modulating, in a host cell, a protein-protein interaction between first  
PT protein, PRAK, (MAPKAPK5) and second protein, ERK3, (extracellular signal  
PT -regulated kinase 3) by administering modulating compound.  
XX Disclosure; SEQ ID NO 39; 296pp; English.  
XX The invention relates to a method for modulating, in a host cell, a  
CC protein-protein interaction between a first protein which is PRAK (P38-  
CC regulated/activated protein kinase or MAPKAPK5) and a second protein  
CC which is ERK3 (extracellular signal-regulated kinase 3). The method  
CC comprises administering to the cell a compound capable of modulating the  
CC protein-protein interaction. The method is useful in modulating in a host  
CC cell a protein-protein interaction between a first protein which is PRAK  
CC and a second protein which is ERK3 for treating inflammation or  
CC inflammatory disorders, e.g., asthma, rheumatoid arthritis, juvenile  
CC chronic arthritis, myositis, Crohn's disease, gastritis, colitis,  
CC ulcerative colitis, inflammatory bowel disease, proctitis, pelvic  
CC inflammatory disease, systemic lupus erythematosus, rhinitis,  
CC conjunctivitis, scleritis, chronic inflammatory polyneuropathy, Tertiary  
CC Lyme disease, psoriasis, dermatitis or eczema. In the exemplification of  
CC the present invention examples of antisense oligonucleotides specific to  
CC nucleic acids encoding individual proteins in tables 1 to 82 are provided  
CC in SEQ ID NOS:11-223 (ADZ97857-ADZ98069).  
XX Sequence 20 BP; 4 A; 10 C; 2 G; 4 T; 0 U; 0 Other;  
SQ Query Match 59.2%; Score 14.2; DB 14; Length 20;  
Best Local Similarity 68.4%; Pred. No. 7.7e+03;  
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
QY 5 AGGGGUGUUUAGGCGUC 23  
DB 20 AGGGGCTGGTAATGAGTC 2  
RESULT 11  
ADJ13347/c  
ID ADJ13347 standard; DNA; 21 BP.  
XX AC ADJ13347;  
XX 20-MAY-2004 (first entry)  
DT Human DNA probe used to immobilise CpG methylated DNA seqid 474.  
XX



KW probe; ss; chemical modification; methylation; array; CpG island;  
 KW tumour suppressor; p16; human; H69; H1618.  
 XX Homo sapiens.  
 OS  
 XX US2003152950-A1.  
 PN  
 XX 14-AUG-2003.  
 PD  
 XX 27-JUN-2002; 2002US-00184085.  
 XX  
 XX 27-JUN-2001; 2001US-0301370P.  
 PR  
 XX (GARN//) GARNER H R.  
 PA (MINN//) MINNA J D.  
 PA (LUEB//) LUEBKE K J.  
 PA (BALO//) BALOG R P.  
 XX  
 XX Garner HR, Minna JD, Luebke KJ, Balog RP;  
 PI WPI; 2003-874843/81.  
 XX  
 XX Analysis of chemical modification of DNA involves obtaining sample of DNA  
 PT to be analyzed, treating DNA with chemical reagents that result in  
 PT different base sequences, and determining sequence of resulting DNA.  
 XX  
 XX Example 1; SEQ ID NO 474; 210pp; English.  
 PS  
 XX This invention relates to a novel method for analysing chemically  
 CC modified macromolecules. Specifically, it refers to a high throughput  
 CC method for the parallel analysis of many potential sites of chemical  
 CC modification (e.g. methylation) in DNA. The present invention describes  
 CC treating the DNA with one or more chemical reagents that result in  
 CC different base sequences depending upon the presence or absence of the  
 CC modification of interest. Accordingly, a device comprising an array of  
 CC probes is provided to hybridise with and select the altered DNA sequences  
 CC that comprise the modifications of interest such as a CpG island. In  
 CC particular, this invention refers to analysing the methylation pattern of  
 CC a region of the promoter for the tumour suppressor gene p16 from two  
 CC human lung tumour cell lines H69 and H1618. This oligonucleotide sequence  
 CC is a human DNA probe used to immobilise CpG methylated DNA of the  
 CC invention.  
 XX  
 XX Sequence 21 BP; 6 A; 11 C; 1 G; 3 T; 0 U; 0 Other;  
 SQ  
 Query Match 59.2%; Score 14.2; DB 11; Length 21;  
 Best Local Similarity 63.2%; Pred. No. 7.7e+03;  
 Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 UGAGAGGGCGGCUUAGG 19  
 DB 20 TGAGGGGTGCTGTGAGG 2  
 RESULT 12  
 AAAA61591  
 ID AAA61591 standard; DNA; 25 BP.  
 XX  
 AC AAA61591;  
 XX  
 XX 23-OCT-2000 (first entry)  
 DT  
 XX Human Tespec PRO-3 5' RACE PCR primer, hPRO3-D.  
 DE  
 XX Human Tespec PRO-3; testis specific serine protease;  
 KW trypsin family serine protease; mature testis; sperm differentiation;  
 KW sperm maturation; male infertility; sterility; reproductive disorder;  
 KW contraception; rapid amplification of cDNA ends; RACE PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 XX WO200026352-A1.  
 PN  
 XX Mittmann MP;

PD 11-MAY-2000.  
 XX  
 XX 02-NOV-1999; 99WO-JP006111.  
 XX  
 XX 04-NOV-1998; 98JP-00313366.  
 XX  
 XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.  
 PA  
 XX Senoo C, Numata M;  
 PI WPI; 2000-365604/31.  
 XX  
 XX Trypsin family serine proteases expressed specifically in mature testis  
 PT for development of methods for diagnosis and treatment of sterility and  
 PT for contraception.  
 XX  
 XX Example 9; Page 45; 121pp; Japanese.  
 PS  
 XX The invention relates to novel murine and human testis specific serine  
 CC proteases (Tespec PRO; AAB03156-B03160) and to cDNAs encoding them  
 CC (AAA61558-A61562). It also encompasses expression vectors and host cells  
 CC comprising a nucleotide sequence encoding a protease of the invention,  
 CC inhibitors of the proteases and antibodies against the proteases. The  
 CC novel proteases are members of the trypsin family of serine proteases,  
 CC having the serine and histidine active site signatures characteristic of  
 CC this family. The proteases are specifically expressed in mature testis  
 CC and participate in the differentiation and maturation of sperm. The  
 CC proteases are potentially useful for the development of pharmaceuticals  
 CC for the treatment of male infertility and other male reproductive  
 CC disorders, and for the development of contraceptives. They may also be  
 CC used as reagents for the diagnosis of male infertility. Sequences  
 CC AAA61590-A61593 represent RACE (rapid amplification of cDNA ends) PCR  
 CC primers used in the isolation of cDNA encoding human Tespec PRO-3  
 CC (AAA61561)  
 XX  
 XX Sequence 25 BP; 4 A; 2 C; 10 G; 9 T; 0 U; 0 Other;  
 SQ  
 Query Match 59.2%; Score 14.2; DB 3; Length 25;  
 Best Local Similarity 63.2%; Pred. No. 7.9e+03;  
 Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 GAGGGCGGCUUAGGCGU 22  
 DB 3 GATGGGCTAGTTAAGTCGT 21  
 RESULT 13  
 AC182777  
 ID AC182777 standard; DNA; 25 BP.  
 XX  
 AC AC182777;  
 XX  
 XX 14-OCT-2003 (first entry)  
 DT  
 XX Human microarray DNA oligonucleotide SEQ ID NO 82768.  
 DE  
 XX EST; ss; probe; expressed sequence tag; microarray; gene expression;  
 KW genetic variation; biallelic marker; polymorphism; human;  
 KW cross-species comparison.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2003104410-A1.  
 PN  
 XX 05-JUN-2003.  
 PD  
 XX 15-MAR-2002; 2002US-00098263.  
 PF  
 XX 16-MAR-2001; 2001US-0276759P.  
 PR  
 XX (AFFY-) AFFYMETRIX INC.  
 PA  
 XX Mittmann MP;

XX WPI; 2003-567953/53.  
XX New array of nucleic acid probes, useful for in situ hybridization, in  
PT Southern, Northern or dot-blot hybridization to identify or detect the  
PT sequence or specific mutations of any gene.  
XX Claim 1; SEQ ID NO 82768; 9pp; English.  
XX  
CC The invention discloses a microarray comprising a plurality of nucleic  
CC acid probes including one of 2,018,500 fully defined sequences, or its  
CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
CC Also disclosed is a method of gene expression analysis. The array is used  
CC in monitoring gene expression levels by hybridisation to a DNA library,  
CC in analysis of genetic variation or in hybridisation of tag-labelled  
CC compounds. The nucleic acid probes are specifically designed for analysis  
CC of at least one target sequence. The method of analysis comprises  
CC hybridising at least one or more nucleic acids to at least two or more  
CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
CC probes are attached to a solid support. The analysis comprises monitoring  
CC gene expression levels, identifying allelic markers or polymorphisms,  
CC or family members of a gene and a cross-species comparison. Each of the  
CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
CC probes is useful in in situ hybridisation in Southern, Northern or dot-  
CC blot hybridisation to identify or detect the sequence or specific  
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
CC primer extensions or in screening cDNA or genomic libraries or subclones  
CC for additional subclones containing segments of DNA that have been  
CC isolated and previously sequenced. The sequence presented is one of the  
CC nucleic acid probes incorporated in the microarray. Note: The sequence  
CC data for this patent can also be obtained in electronic format directly  
CC from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)  
XX  
SQ Sequence 25 BP; 6 A; 4 C; 10 G; 5 T; 0 U; 0 Other;  
Query Match 58.3%; Score 14; DB 9; Length 25;  
Best Local Similarity 59.1%; Pred. No. 9.8e+03;  
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
QY 2 GACAGGGGCGUGUUAAGCGUC 23  
DB 1 GACAGGGGATCGTTAGACGTC 22  
RESULT 14  
ACD57816/c  
ID ACD57816 standard; RNA; 17 BP.  
XX  
AC ACD57816;  
XX  
DT 23-SEP-2003 (first entry)  
XX  
DE HCV DNzyme substrate sequence #514.  
XX  
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
KW RNA stability; RNA expression; RNA synthesis; antisense;  
KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;  
KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
KW HBV reverse transcriptase; Enhancer I region; viral replication;  
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
KW virucide; antiinflammatory; substrate; ss.  
XX  
OS Hepatitis C virus.  
XX  
XX WO200281494-A1.  
XX  
XX 17-OCT-2002.  
XX  
XX 26-MAR-2002; 2002WO-US009187.  
XX  
XX 26-MAR-2001; 2001US-00817879.  
XX  
XX 08-JUN-2001; 2001US-00877478.  
XX  
PR  
PR 08-JUN-2001; 2001US-0296876P.  
PR 24-OCT-2001; 2001US-0335059P.  
PR 05-DEC-2001; 2001US-0337055P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MACE/) MACEJAK D.  
PA (MCSW/) MCSWIGGEN J.  
PA (MORR/) MORRISSEY D.  
PA (PAVC/) PAVCO P.  
PA (LEEP/) LEE P.  
PA (DRAP/) DRAPER K.  
PA (ROBE/) ROBERTS E.  
XX  
PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
PI Draper K, Roberts E;  
XX WPI; 2003-229207/22.  
XX  
XX Novel compound useful for treating cirrhosis, liver failure,  
PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
PT infection.  
XX  
PS Claim 1; Page 243; 387pp; English.  
XX  
CC The present invention relates to nucleic acid molecules which modulate  
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNzymes,  
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
CC DNA. The nucleic acids may be used to modulate the expression of HBV  
CC genes and HBV viral replication. Also disclosed is a method for screening  
CC compounds and/or potential therapies directed against HBV, and compounds  
CC that modulate the expression and/or replication of HCV. The compounds and  
CC methods of the invention are useful for the treatment of degenerative and  
CC disease states related to HBV and HCV infection, replication and gene  
CC expression such as cirrhosis, liver failure, and hepatocellular  
CC carcinoma. The present sequence represents a substrate for one of the HCV  
CC DNzyme or minus strand DNzyme sequences disclosed in the present  
CC invention  
XX  
SQ Sequence 17 BP; 4 A; 9 C; 1 G; 0 T; 3 U; 0 Other;  
Query Match 57.5%; Score 13.8; DB 8; Length 17;  
Best Local Similarity 70.6%; Pred. No. 1.2e+04;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 6 GGGCGUGGUUAGGCGU 22  
DB 17 GGGCAGGTTAGGTGT 1  
RESULT 15  
AD183268/c  
ID AD183268 standard; RNA; 17 BP.  
XX  
AC AD183268;  
XX  
DT 22-SEP-2005 (revised)  
DT 03-JUN-2004 (first entry)  
XX  
XX HCV DNzyme substrate sequence #514.  
DE  
XX ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;  
KW HCV infection; type I interferon; DNzyme.  
XX  
OS Hepatitis C virus.  
XX  
XX US2003125270-A1.  
XX  
XX

```

PD 03-JUL-2003.
XX
XX 18-DEC-2000; 2000US-00740332.
XX
XX 18-DEC-2000; 2000US-00740332.
XX
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J.
XX (ROBE/) ROBERTS E.
XX (PAVC/) PAVCO P A.
XX (MACE/) MACEJACK D.
XX
XX Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;
XX WPI; 2004-031273/03.
XX
XX Enzymatic nucleic acid molecules which specifically cleave RNA derived
XX from hepatitis C virus (HCV), useful for the treatment of HCV infections,
XX especially in combination with type I interferon therapy.
XX
XX Claim 1; SEQ ID NO 514; 198pp; English.
XX
XX The invention relates to an enzymatic nucleic acid molecule which
XX specifically cleaves RNA derived from hepatitis C virus (HCV), in which
XX the binding arms of the enzymatic nucleic acid molecule comprises
XX sequences complementary to any of the defined substrate sequences given
XX in the specification. The nucleic acid molecule may be administered for
XX the treatment of HCV infections, especially in combination with type I
XX interferons. The present sequence represents a HCV DNAzyme substrate
XX sequence.
XX
XX Revised record issued on 22-SEP-2005 : No correction was made to this
XX record
XX
XX Sequence 17 BP; 4 A; 9 C; 1 G; 0 T; 3 U; 0 Other;
XX
XX
XX Query Match 57.5%; Score 13.8; DB 12; Length 17;
XX Best Local Similarity 70.6%; Pred.No. 1.2e+04;
XX Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 6 GGGGCGUGUAGGCGU 22
XX ||||| |||||
XX 17 GGGGCGGTTAAGGTGT 1
XX
XX Search completed: June 19, 2007, 13:01:30
XX Job time : 249.5 secs

```

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 12:53:27 ; Search time 256 Seconds  
(without alignments)  
175.760 Million cell updates/sec

Title: US-10-604-726A-6034  
Perfect score: 24  
Sequence: 1 usagaggggucguuaagcgucc 24

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 960512

Minimum DB seq length: 0  
Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_NA.\*  
1: /EMC Celerra\_SIDS3/ptodata/2/ina/1 COMB.seq.\*  
2: /EMC Celerra\_SIDS3/ptodata/2/ina/5 COMB.seq.\*  
3: /EMC Celerra\_SIDS3/ptodata/2/ina/6A COMB.seq.\*  
4: /EMC Celerra\_SIDS3/ptodata/2/ina/6B COMB.seq.\*  
5: /EMC Celerra\_SIDS3/ptodata/2/ina/7 COMB.seq.\*  
6: /EMC Celerra\_SIDS3/ptodata/2/ina/H COMB.seq.\*  
7: /EMC Celerra\_SIDS3/ptodata/2/ina/PCTUS COMB.seq.\*  
8: /EMC Celerra\_SIDS3/ptodata/2/ina/PP COMB.seq.\*  
9: /EMC Celerra\_SIDS3/ptodata/2/ina/RE COMB.seq.\*  
10: /EMC Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	14	58.3	25	3	US-09-396-196G-15707
C 2	13.8	57.5	22	2	US-08-179-738-12
C 3	13.8	57.5	22	2	US-08-628-145-12
C 4	13.2	55.0	25	2	US-08-295-814E-23
C 5	13.2	55.0	25	3	US-09-343-361-23
C 6	12.8	53.3	19	2	US-08-460-751-27
C 7	12.8	53.3	25	3	US-09-641-259B-31
C 8	12.6	52.5	19	3	US-09-059-579A-123
C 9	12.6	52.5	20	3	US-09-166-186-119
C 10	12.6	52.5	20	3	US-09-313-932-119
C 11	12.6	52.5	20	3	US-09-980-052-51
C 12	12.6	52.5	21	3	US-08-520-373D-31
C 13	12.6	52.5	25	3	US-09-443-067-45
C 14	12.6	52.5	25	3	US-09-396-196G-3644
C 15	12.6	52.5	25	3	US-09-396-196G-29254
C 16	12.4	51.7	24	3	US-09-630-377-11
C 17	12.4	51.7	25	3	US-09-396-196G-41852
C 18	12.4	51.7	25	3	US-09-396-196G-58488
C 19	12.4	51.7	25	3	US-09-396-196G-73489
C 20	12.4	51.7	25	3	US-09-396-196G-78586
C 21	12.4	51.7	25	3	US-09-396-196G-122139
C 22	12.4	51.7	25	3	US-09-396-196G-122140
C 23	12.2	50.8	19	3	US-09-422-978-9132

24	12.2	50.8	20	2	US-08-117-952-440	Sequence 440, Appl
25	12.2	50.8	20	3	US-09-526-193A-6	Sequence 6, Appli
26	12.2	50.8	20	3	US-09-526-193A-82	Sequence 82, Appl
27	12.2	50.8	21	3	US-09-553-231-3	Sequence 3, Appli
C 28	12.2	50.8	21	3	US-09-657-472-264	Sequence 264, App
29	12.2	50.8	21	3	US-09-553-231-3	Sequence 3, Appli
30	12.2	50.8	21	5	US-10-161-849-3	Sequence 3, Appli
31	12	50.0	21	3	US-09-328-174A-66	Sequence 66, Appl
32	12	50.0	21	3	US-09-735-271-1593	Sequence 1593, Ap
C 33	12	50.0	22	2	US-08-519-197-7	Sequence 7, Appli
C 34	12	50.0	22	3	US-09-930-218-7	Sequence 14034, A
35	12	50.0	25	3	US-09-396-196G-14034	Sequence 42202, A
C 36	12	50.0	25	3	US-09-396-196G-44091	Sequence 44091, A
C 37	12	50.0	25	3	US-09-396-196G-4032	Sequence 4032, Ap
C 38	11.8	49.2	18	3	US-09-371-772B-4032	Sequence 4032, Ap
C 39	11.8	49.2	18	3	US-09-685-664B-4032	Sequence 4032, Ap
C 40	11.8	49.2	18	3	US-10-138-674B-4032	Sequence 4032, Ap
C 41	11.8	49.2	18	5	US-10-530-492-152	Sequence 152, App
C 42	11.8	49.2	20	2	US-08-506-517-152	Sequence 152, App
C 43	11.8	49.2	20	3	US-08-576-202-35	Sequence 35, Appli
C 44	11.8	49.2	20	3	US-09-076-259-2	Sequence 2, Appli
C 45	11.8	49.2	20	3		

## ALIGNMENTS

RESULT 1  
US-09-396-196G-15707/C  
; Sequence 15707, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15707  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-396-196G-15707

Query Match 58.3%; Score 14; DB 3; Length 25;  
Best Local Similarity 54.5%; Pred. No. 2e+03;  
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 UGAGAGGGGCGUGUUAAGCGU 22  
Db 22 TGAGATGAGCTGCTTACGAGT 1

RESULT 2  
US-08-179-738-12/c  
; Sequence 12, Application US/08179738  
; Patent No. 5578462  
; GENERAL INFORMATION:  
; APPLICANT: Seizinger, Bernd R.  
; APPLICANT: Kley, Nikolai A.  
; APPLICANT: Bianchi, Albert B.  
; TITLE OF INVENTION: No. 5578462el NF2 Isoforms  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Reed & Robins  
; STREET: 635 Bryant Street  
; CITY: Palo Alto

STATE: California  
COUNTRY: U.S.A  
ZIP: 94301  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/179,738  
FILING DATE: 10-JAN-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Robins, Roberta L.  
REGISTRATION NUMBER: 33,208  
REFERENCE/DOCKET NUMBER: 5998-0017  
TELEPHONE: (415) 617-8999  
TELEFAX: (415) 327-3231  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-179-738-12

Query Match 57.5%; Score 13.8; DB 2; Length 22;  
Best Local Similarity 70.6%; Pred. No. 2.5e+03;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGAGGGCUGGUUAGG 19  
|||||:|:|:|:|:|  
Db 17 AGAGGAGCTGTTTCAGG 1

RESULT 3  
US-08-628-145-12/c  
; Sequence 12, Application US/08628145  
; Patent No. 5872214  
; GENERAL INFORMATION:  
; APPLICANT: Seizinger, Bernd R.  
; APPLICANT: Kley, Nikolai A.  
; APPLICANT: Bianchi, Albert B.  
; TITLE OF INVENTION: No. 5872214el NF2 Isoforms  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Reed & Robins  
; STREET: 635 Bryant Street  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: U.S.A  
; ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/628,145  
FILING DATE: 04-APR-1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/179,738  
FILING DATE: 10-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Robins, Roberta L.  
REGISTRATION NUMBER: 33,208  
REFERENCE/DOCKET NUMBER: 5998-0017  
TELEPHONE: (415) 617-8999  
TELEFAX: (415) 327-3231

INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-628-145-12  
Query Match 57.5%; Score 13.8; DB 2; Length 22;  
Best Local Similarity 70.6%; Pred. No. 2.5e+03;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGAGGGCUGGUUAGG 19  
|||||:|:|:|:|:|  
Db 17 AGAGGAGCTGTTTCAGG 1

RESULT 4  
US-08-295-814E-23/c  
; Sequence 23, Application US/08295814E  
; Patent No. 5658786  
; GENERAL INFORMATION:  
; APPLICANT: Smith, Kelli E.  
; APPLICANT: Borden, Laurence A.  
; APPLICANT: Hartig, Paul R.  
; APPLICANT: Weinschenk, Richard L.  
; TITLE OF INVENTION: DNA ENCODING TAURINE AND GABA  
; TITLE OF INVENTION: TRANSPORTERS AND USES THEREOF  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/295,814E  
FILING DATE: DECEMBER 19, 1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 40558-B-PCT-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0525  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-295-814E-23

Query Match 55.0%; Score 13.2; DB 2; Length 25;  
Best Local Similarity 66.7%; Pred. No. 4.9e+03;  
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 5 AGGGGCGUGGUUAGGCGU 22  
|||||:|:|:|:|:|  
Db 23 AGGTGCTGCTGAGGCGAT 6

RESULT 5  
US-09-343-361-23/c

US-08-460-751-27

Query Match 53.3%; Score 12.8; DB 2; Length 19;  
Best Local Similarity 62.5%; Pred. No. 7.3e+03;  
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCUGGUUAGGCGUCC 24  
||: :|||||:|  
DB 1 GCTCTTAAAGCGGTC 16

RESULT 7  
US-09-641-259B-31/c  
; Sequence 31, Application US/09641259B  
; Patent No. 6468756  
; GENERAL INFORMATION:  
; APPLICANT: Bonini, James A  
; APPLICANT: Borowsky, Beth E  
; APPLICANT: Adham, Nika  
; APPLICANT: Boyle, No. 64687561  
; APPLICANT: Thompson, Thelma O.  
; TITLE OF INVENTION: DNA Encoding SNORF25 Receptor  
; FILE REFERENCE: 1795/56095-B/JPW/ADM  
; CURRENT APPLICATION NUMBER: US/09/641,259B  
; CURRENT FILING DATE: 2002-03-12  
; PRIOR APPLICATION NUMBER: PCT/US00/04413  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 09/387,699  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: US 09/255,376  
; PRIOR FILING DATE: 1999-02-22  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 31  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer/ Probe  
US-09-641-259B-31

Query Match 53.3%; Score 12.8; DB 3; Length 25;  
Best Local Similarity 68.8%; Pred. No. 7.6e+03;  
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGGGCGUGGUUAGG 19  
|||||:|:|  
DB 20 GAGGGCGTCTTAATG 5

RESULT 8  
US-10-059-579A-123/c  
; Sequence 123, Application US/10059579A  
; Patent No. 6835541  
; GENERAL INFORMATION:  
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
; APPLICANT: SUKIMAR, Sarawati  
; APPLICANT: EVRON, Ella  
; APPLICANT: DOOLEY, William C.  
; APPLICANT: DAVIDSON, Nancy  
; APPLICANT: FACKLER, Mary Jo.  
; TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY  
; FILE REFERENCE: JHU1630-1  
; CURRENT APPLICATION NUMBER: US/10/059,579A  
; CURRENT FILING DATE: 2002-01-28  
; PRIOR APPLICATION NUMBER: US 09/771,357  
; PRIOR FILING DATE: 2001-01-26  
; NUMBER OF SEQ ID NOS: 136  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 123  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial sequence

Qy 4 GAGGGCUGGUTUAAGCGU 22

```

CURRENT FILING DATE: 1995-08-29
PRIORITY APPLICATION NUMBER: 08/377,710
PRIORITY FILING DATE: 1995-01-25
PRIORITY APPLICATION NUMBER: 08/279,979
PRIORITY FILING DATE: 1994-07-25
PRIORITY APPLICATION NUMBER: 07/894,215
PRIORITY FILING DATE: 1992-06-04
PRIORITY APPLICATION NUMBER: 07/952,796
PRIORITY FILING DATE: 1992-09-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
LENGTH: 21

```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PRIMER
; OTHER INFORMATION: PRIMER 1
US-08-520-373D-31

Query Match      52.5%; Score 12.6; DB 3; Length 21;
Best Local Similarity 63.2%; Pred. No. 9.2e+03;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      3 AGAGGGGCGUUAAGGCG 21
Db      19 ATAAAGGCTGTTAAGGTG 1

RESULT 13
US-09-443-067-45
; Sequence 45, Application US/09443067
; Patent No. 6627794
; GENERAL INFORMATION:
; APPLICANT: COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH
; APPLICANT: ORGANISATION
; TITLE OF INVENTION: Polyphenol oxidase genes from banana, lettuce, tobacco and
; TITLE OF INVENTION: pineapple
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,067
; CURRENT FILING DATE: 1999-11-18
; EARLIER APPLICATION NUMBER: US 08/976, 222
; EARLIER FILING DATE: 1997-11-21
; EARLIER APPLICATION NUMBER: PCT/AU98/00362
; EARLIER FILING DATE: 1998-05-19
; EARLIER APPLICATION NUMBER: AU PP3898
; EARLIER FILING DATE: 1995-05-23
; EARLIER APPLICATION NUMBER: AU PP6849
; EARLIER FILING DATE: 1997-05-19
; EARLIER APPLICATION NUMBER: AU PP5600
; EARLIER FILING DATE: 1995-09-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-443-067-45

Query Match      52.5%; Score 12.6; DB 3; Length 25;
Best Local Similarity 63.2%; Pred. No. 9.5e+03;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      5 AGGGGCGUUAAGGCGUC 23
Db      6 ATGGGATGCTGAAGGTGTC 24

RESULT 14
US-09-396-196G-3644/c
; Sequence 3644, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
```

```
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3644
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-3644

Query Match      52.5%; Score 12.6; DB 3; Length 25;
Best Local Similarity 68.4%; Pred. No. 9.5e+03;
Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      3 AGAGGGGCGUUAAGGCG 21
Db      21 AGAGAGTCTGGTGAAGCG 3

RESULT 15
US-09-396-196G-29254
; Sequence 29254, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29254
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-29254

Query Match      52.5%; Score 12.6; DB 3; Length 25;
Best Local Similarity 57.9%; Pred. No. 9.5e+03;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      1 UGAGAGGGGCGUUAAGG 19
Db      7 TCAGAGGGCGCTAGTTATG 25

Search completed: June 19, 2007, 13:10:06
Job time : 256.5 secs
```



GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 13:01:01 ; Search time 1262 Seconds  
(without alignments)  
233.679 Million cell updates/sec

Title: US-10-604-726a-6034

Perfect score: 24  
Sequence: 1 usagagggcuguaagcgucc 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 22906428

Minimum DB seq length: 0  
Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA Main:

- 1: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 2: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 3: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 4: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 5: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 6: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US09D\_PUBCOMB.seq.\*
- 7: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
- 8: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 9: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 10: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*
- 11: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*
- 12: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*
- 13: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*
- 14: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*
- 15: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US11B\_PUBCOMB.seq.\*
- 16: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US11C\_PUBCOMB.seq.\*
- 17: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US11D\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	16.6	69.2	25	13	US-11-036-317-713202
C 2	16.2	67.5	25	9	US-10-719-900-888593
C 3	15.8	65.8	24	3	US-09-940-185-365
C 4	15.8	65.8	25	3	US-09-940-185-4341
C 5	15.8	65.8	25	13	US-11-036-317-751276
C 6	15.6	65.0	25	13	US-11-036-317-508584
C 7	15.6	65.0	25	13	US-11-036-317-648052
C 8	15.2	63.3	21	11	US-10-310-914A-310484
C 9	15.2	63.3	21	11	US-10-310-914A-310485
C 10	15.2	63.3	21	11	US-10-310-914A-310486
C 11	15.2	63.3	21	11	US-10-310-914A-310487
C 12	15.2	63.3	21	11	US-10-310-914A-594029
C 13	15.2	63.3	21	11	US-10-310-914A-1286104
C 14	15.2	63.3	22	11	US-10-310-914A-1056699
C 15	15.2	63.3	22	11	US-10-310-914A-594065
C 16	15.2	63.3	24	11	US-10-310-914A-1286102
C 17	15.2	63.3	25	9	US-10-719-900-623329

18	15.2	63.3	25	15	US-11-121-849-463132	Sequence 463132,
C 19	15	62.5	25	9	US-10-719-900-470368	Sequence 470368,
20	15	62.5	25	13	US-11-036-317-537085	Sequence 473457,
C 21	15	62.5	25	13	US-11-036-317-537085	Sequence 537085,
C 22	15	62.5	25	13	US-11-036-317-657262	Sequence 657262,
C 23	15	62.5	25	13	US-11-036-317-713203	Sequence 713203,
C 24	15	62.5	25	13	US-11-036-317-798014	Sequence 798014,
C 25	14.8	61.7	21	11	US-10-310-914A-752575	Sequence 752575,
C 26	14.6	61.7	22	11	US-10-310-914A-175870	Sequence 175870,
C 27	14.6	60.8	21	11	US-10-310-914A-371120	Sequence 371120,
C 28	14.6	60.8	23	11	US-10-310-914A-707100	Sequence 707100,
C 29	14.6	60.8	23	11	US-10-310-914A-1006052	Sequence 1006052,
C 30	14.6	60.8	24	9	US-10-469-866-23	Sequence 23, Appl
C 31	14.6	60.8	24	11	US-10-310-914A-224322	Sequence 224322,
C 32	14.6	60.8	25	8	US-10-719-956-115625	Sequence 115625,
C 33	14.6	60.8	25	8	US-10-719-956-115627	Sequence 115627,
C 34	14.6	60.8	25	9	US-10-719-900-888594	Sequence 888594,
C 35	14.6	60.8	25	13	US-11-036-317-892224	Sequence 892224,
C 36	14.6	60.8	25	13	US-11-036-317-966783	Sequence 966783,
C 37	14.6	60.8	25	13	US-11-121-849-363	Sequence 363, App
C 38	14.4	60.0	21	12	US-10-504-589A-7	Sequence 7, Appli
C 39	14.4	60.0	24	11	US-10-310-914A-1339473	Sequence 1339473,
C 40	14.4	60.0	25	8	US-10-719-956-605791	Sequence 605791,
C 41	14.4	60.0	25	8	US-10-719-956-605792	Sequence 605792,
C 42	14.4	60.0	25	13	US-11-036-317-213436	Sequence 213436,
C 43	14.4	60.0	25	13	US-11-036-317-884459	Sequence 884459,
C 44	14.2	59.2	19	11	US-10-310-914A-1056695	Sequence 1056695,
C 45	14.2	59.2	19	14	US-11-083-784-1176587	Sequence 1176587,

## ALIGNMENTS

### RESULT 1

US-11-036-317-713202/c  
; Sequence 713202, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036.317  
; CURRENT FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639  
; PRIOR FILING DATE: 2004-01-13  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 713202  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-713202

Query Match	69.2%	Score	16.6;	DB	13;	Length	25;
Best Local Similarity	65.2%	Pred. No.	8.8e+02;				
Mismatches	15;	Conservative	4;	Mismatches	4;	Indels	0;
						Gaps	0;

### RESULT 2

US-10-719-900-888593/c  
; Sequence 888593, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20

```
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 888593
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-888593

Query Match      67.5%; Score 16.2; DB 9; Length 25;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY  4 GAGGGGCGUGUUAAGCGGUCC 24
    |||||:|:|:|:|:|:|:|:|:|
DB  23 GAGGGCTAGTTAAGGCTTCC  3

RESULT 3
US-09-940-185-365
; Sequence 365, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 365
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-365

Query Match      65.8%; Score 15.8; DB 3; Length 24;
Best Local Similarity 73.7%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY  2 GAGAGGGCGUGGUUAAGGC 20
    |||||:|:|:|:|:|:|:|
DB  4 GAGAGGCGTTGGTTAAGGC 22

RESULT 4
US-09-940-185-4341
; Sequence 4341, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4341
; LENGTH: 25
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-4341

Query Match      65.8%; Score 15.8; DB 3; Length 25;
Best Local Similarity 73.7%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY  2 GAGAGGGCGUGGUUAAGGC 20
    |||||:|:|:|:|:|:|:|
DB  5 GAGAGGCGTTGGTTAAGGC 23

RESULT 5
US-11-036-317-751276/c
; Sequence 751276, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 751276
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-751276

Query Match      65.8%; Score 15.8; DB 13; Length 25;
Best Local Similarity 68.4%; Pred. No. 2.1e+03;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY  1 UGAGAGGGCGUGGUUAAGG 19
    :|:|:|:|:|:|:|:|:|
DB  25 TCAAAGGGCGCTGGTTAAGG  7

RESULT 6
US-11-036-317-508584/c
; Sequence 508584, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 508584
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-508584

Query Match      65.0%; Score 15.6; DB 13; Length 25;
Best Local Similarity 63.6%; Pred. No. 2.6e+03;
Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY  3 AGAGGGCGUGGUUAAGCGUCC 24
    |||||:|:|:|:|:|:|:|
DB  25 AGAGGGCGCTGGTTCAAGGATCC  4
```

```
RESULT 7
US-11-036-317-648052/c
; Sequence 648052, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036.317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 648052
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-648052

Query Match      65.0%; Score 15.6; DB 13; Length 25;
Best Local Similarity 63.6%; Pred. No. 2.6e+03;
Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy  2  GAGAGGGCGCGUUAAGGCGUC 23
      |||||  |||||  |||||  |||||  |||||
Db  22 GAGAGGCCCTGTTCAAGGAGTC 1

RESULT 8
US-10-310-914A-310484/c
; Sequence 310484, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuizat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 310484
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-310484

Query Match      63.3%; Score 15.2; DB 11; Length 21;
Best Local Similarity 75.0%; Pred. No. 4.1e+03;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy  1  UGAGAGGGCGUGGUUAGGC 20
      :|||||  |||||  |||||  |||||  |||||
Db  21 TGAGAGGGGAAGGCTAAGGC 2

RESULT 9
US-10-310-914A-310485/c
; Sequence 310485, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuizat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
```

```
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 310485
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-310485

Query Match      63.3%; Score 15.2; DB 11; Length 21;
Best Local Similarity 75.0%; Pred. No. 4.1e+03;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy  1  UGAGAGGGCGUGGUUAGGC 20
      :|||||  |||||  |||||  |||||  |||||
Db  21 TGAGAGGGGAAGGCTAAGGC 2

RESULT 10
US-10-310-914A-310486/c
; Sequence 310486, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuizat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 310486
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-310486

Query Match      63.3%; Score 15.2; DB 11; Length 21;
Best Local Similarity 75.0%; Pred. No. 4.1e+03;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy  1  UGAGAGGGCGUGGUUAGGC 20
      :|||||  |||||  |||||  |||||  |||||
Db  21 TGAGAGGGGAAGGCTAAGGC 2

RESULT 11
US-10-310-914A-310487/c
; Sequence 310487, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuizat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 310487
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-310487

Query Match      63.3%; Score 15.2; DB 11; Length 21;
Best Local Similarity 75.0%; Pred. No. 4.1e+03;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy  1  UGAGAGGGCGUGGUUAGGC 20
      :|||||  |||||  |||||  |||||  |||||
Db  21 TGAGAGGGGAAGGCTAAGGC 2
```

## RESULT 12

US-10-310-914A-594029  
; Sequence 594029, Application US/10310914A  
; Publication No. US20060003322A1

## ; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; TITLE OF INVENTION: uses thereof

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 594029

; LENGTH: 21

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-594029

Query Match 63.3%; Score 15.2; DB 11; Length 21;

Best Local Similarity 85.0%; Pred. No. 4.1e+03;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAGAGGGCGUGGUUAAAGCG 21

Db 2 GAGAGGGCGUGGUUGGGUG 21

## RESULT 13

US-10-310-914A-1286104/c  
; Sequence 1286104, Application US/10310914A  
; Publication No. US20060003322A1

## ; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; TITLE OF INVENTION: uses thereof

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 1286104

; LENGTH: 21

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-1286104

Query Match 63.3%; Score 15.2; DB 11; Length 21;

Best Local Similarity 80.0%; Pred. No. 4.1e+03;

Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAGAGGGCGUGGUUAAAGCG 21

Db 21 GAGAGGGCTGGAGAGGCG 2

## RESULT 14

US-10-310-914A-1056699/c  
; Sequence 1056699, Application US/10310914A  
; Publication No. US20060003322A1

## ; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; TITLE OF INVENTION: uses thereof

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 1056699

; LENGTH: 22

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-1056699

Query Match 63.3%; Score 15.2; DB 11; Length 22;

Best Local Similarity 80.0%; Pred. No. 4.1e+03;

Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAGAGGGCGUGGUUAAAGCG 21

Db 21 GAGAGGGCTGGAGAGGCG 2

## RESULT 15

US-10-310-914A-594065  
; Sequence 594065, Application US/10310914A  
; Publication No. US20060003322A1

## ; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; TITLE OF INVENTION: uses thereof

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 594065

; LENGTH: 24

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-594065

Query Match 63.3%; Score 15.2; DB 11; Length 24;

Best Local Similarity 85.0%; Pred. No. 4.1e+03;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAGAGGGCGUGGUUAAAGCG 21

Db 4 GAGAGGGCGUGGUUGGGUG 23

Search completed: June 19, 2007, 16:27:48

Job time : 1263 secs

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 13:01:51 ; Search time 610 Seconds  
(without alignments)  
405.912 Million cell updates/sec

Title: US-10-604-726A-6034

Perfect score: 24

Sequence: 1 ugagagggcgguaagcgucc 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 15754707 seqs, 5162687648 residues

Total number of hits satisfying chosen parameters: 17957554

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq1.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq2.\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq3.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq4.\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq5.\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq6.\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq1.\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq2.\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq3.\*
- 17: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq4.\*
- 18: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq5.\*
- 19: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq6.\*
- 20: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq7.\*
- 21: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq8.\*
- 22: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.2	63.3	25	11	US-10-956-160-156795
2	15.2	63.3	25	11	US-10-956-160-157603
3	14.8	61.7	25	11	US-10-956-160-123988
C 4	14.4	60.0	17	9	US-10-709-691B-1378586
5	14.2	59.2	19	10	US-10-714-333A-1176587
6	14.2	59.2	19	17	US-11-093-832-1176587
C 7	14	58.3	22	9	US-10-709-691B-19539
C 8	14	58.3	22	9	US-10-709-691B-101448
C 9	14	58.3	22	9	US-10-709-691B-123481
C 10	14	58.3	22	9	US-10-709-691B-134127
C 11	14	58.3	22	9	US-10-709-691B-142124

C 12	14	58.3	22	9	US-10-709-691B-145999
C 13	14	58.3	22	9	US-10-709-691B-153005
C 14	14	58.3	22	9	US-10-709-691B-187400
C 15	14	58.3	22	9	US-10-709-691B-197873
C 16	14	58.3	22	9	US-10-709-691B-208809
C 17	14	58.3	22	9	US-10-709-691B-248124
C 18	13.8	57.5	19	10	US-10-714-333A-494904
C 19	13.8	57.5	19	17	US-11-093-832-494904
C 20	13.8	57.5	22	9	US-10-709-691B-42828
C 21	13.8	57.5	22	9	US-10-709-691B-225295
C 22	13.8	57.5	25	9	US-10-859-198-254645
C 23	13.8	57.5	25	14	US-11-217-529-40910
C 24	13.6	56.7	21	13	US-11-509-413-2704
C 25	13.6	56.7	21	13	US-11-509-413-2706
C 26	13.6	56.7	21	13	US-11-509-413-4136
C 27	13.6	56.7	22	19	US-11-130-645A-11011
C 28	13.4	55.8	18	8	US-10-709-691B-1899145
C 29	13.4	55.8	18	8	US-10-709-691B-1969471
C 30	13.4	55.8	19	8	US-10-709-691B-1890291
C 31	13.4	55.8	19	8	US-10-709-691B-1890632
C 32	13.4	55.8	19	8	US-10-709-691B-1899146
C 33	13.4	55.8	19	8	US-10-709-691B-1956798
C 34	13.4	55.8	19	8	US-10-709-691B-1962777
C 35	13.4	55.8	19	8	US-10-709-691B-1969470
C 36	13.4	55.8	19	8	US-10-709-691B-2612611
C 37	13.4	55.8	19	9	US-10-709-691B-578997
C 38	13.4	55.8	19	10	US-10-714-333A-1365090
C 39	13.4	55.8	19	11	US-10-714-333A-46028
C 40	13.4	55.8	19	11	US-10-714-333A-46048
C 41	13.4	55.8	19	17	US-11-093-832-46028
C 42	13.4	55.8	19	17	US-11-093-832-46048
C 43	13.4	55.8	19	17	US-11-093-832-1365090
C 44	13.4	55.8	20	8	US-10-709-691B-1892935
C 45	13.4	55.8	20	8	US-10-709-691B-1893092

#### ALIGNMENTS

RESULT 1  
US-10-956-160-156795  
; Sequence 156795, Application US/10956160  
; Publication No. US20070009899A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL  
; TITLE OF INVENTION: MODELS OF INFLAMMATORY DISEASES  
; FILE REFERENCE: 031896-044000 (AM101084)  
; CURRENT APPLICATION NUMBER: US/10/956,160  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 222274  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 156795  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-10-956-160-156795

Query Match 63.3%; Score 15.2; DB 11; Length 25;  
Best Local Similarity 70.0%; Pred. No. 4.9e+03;  
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 4 GAGGGCGGUGUUAAGCGGUC 23  
|||||:|:|||||  
Db 5 GAGGGACTGCTTAAGCGCAC 24

RESULT 2  
US-10-956-160-157603  
; Sequence 157603, Application US/10956160  
; Publication No. US20070009899A1  
; GENERAL INFORMATION:

; APPLICANT: Wyeth  
 ; APPLICANT: Mounts, William M  
 ; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL  
 ; TITLE OF INVENTION: MODELS OF INFLAMMATORY DISEASES  
 ; FILE REFERENCE: 031896-044000 (AM101084)  
 ; CURRENT APPLICATION NUMBER: US/10/956,160  
 ; CURRENT FILING DATE: 2004-10-04  
 ; NUMBER OF SEQ ID NOS: 222274  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 157603  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Canis familiaris  
 US-10-956-160-157603

Query Match 63.3%; Score 15.2; DB 11; Length 25;  
 Best Local Similarity 70.0%; Pred. No. 4.9e+03;  
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 GAGGGCGUGGUAAGGCGUC 23  
 |||||:|:|||||  
 Db 2 GAGGACTGCTTAGGCGAC 21

RESULT 3  
 US-10-956-160-123988  
 ; Sequence 123988, Application US/10956160  
 ; Publication No. US20070009899A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wyeth  
 ; APPLICANT: Mounts, William M  
 ; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL  
 ; TITLE OF INVENTION: MODELS OF INFLAMMATORY DISEASES  
 ; FILE REFERENCE: 031896-044000 (AM101084)  
 ; CURRENT APPLICATION NUMBER: US/10/956,160  
 ; CURRENT FILING DATE: 2004-10-04  
 ; NUMBER OF SEQ ID NOS: 222274  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 123988  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Canis familiaris  
 US-10-956-160-123988

Query Match 61.7%; Score 14.8; DB 11; Length 25;  
 Best Local Similarity 72.2%; Pred. No. 7.5e+03;  
 Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGGGCGUGGUAAGGCG 21  
 |||||:|:|||||  
 Db 8 GAGGACTGCTTAGGCG 25

RESULT 4  
 US-10-709-691B-1378586/c  
 ; Sequence 1378586, Application US/10709691B  
 ; Publication No. US20070031843A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ROSETTA GENOMICS LTD  
 ; APPLICANT: Bentwich, Itzhak  
 ; APPLICANT: Avniel, Amir  
 ; TITLE OF INVENTION: Bioinformatically Detectable Group of Novel Regulatory Bacterial  
 ; TITLE OF INVENTION: and Bacterial Associated Oligonucleotides and Uses Thereof  
 ; FILE REFERENCE: Efe23  
 ; CURRENT APPLICATION NUMBER: US/10/709,691B  
 ; CURRENT FILING DATE: 2004-05-24  
 ; NUMBER OF SEQ ID NOS: 4254815  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 1378586  
 ; LENGTH: 17  
 ; TYPE: RNA  
 ; ORGANISM: Neisseria meningitidis Z2491  
 US-10-709-691B-1378586

Query Match 60.0%; Score 14.4; DB 9; Length 17;  
 Best Local Similarity 75.0%; Pred. No. 1.1e+04;  
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGGCGUGGUAAGGCG 21  
 |||||:|:|||||  
 Db 17 GGGGCTGGTTACGCG 2

RESULT 5  
 US-10-714-333A-1176587  
 ; Sequence 1176587, Application US/10714333A  
 ; Publication No. US20070031844A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/10/714,333A  
 ; CURRENT FILING DATE: 2003-11-14  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 1176587  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-10-714-333A-1176587

Query Match 59.2%; Score 14.2; DB 10; Length 19;  
 Best Local Similarity 84.2%; Pred. No. 1.4e+04;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGGGCGUGGUAAGGC 20  
 |||||:|:|||||  
 Db 1 GAGAGCAGCUGGUAAGC 19

RESULT 6  
 US-11-093-832-1176587  
 ; Sequence 1176587, Application US/11093832  
 ; Publication No. US20070039072A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/093,832  
 ; CURRENT FILING DATE: 2005-03-29  
 ; PRIOR APPLICATION NUMBER: US/10/714,333  
 ; PRIOR FILING DATE: 2003-11-14  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 1176587  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens

US-10-709-691B-123481/c

; SEQ ID NO 142124  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-709-691B-142124

Query Match 58.3%; Score 14; DB 9; Length 22;  
Best Local Similarity 78.6%; Pred. No. 1.8e+04;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGGGCGUGUUAAG 18  
|||||:|:|:|  
Db 16 AGGGGCTGGTTAAG 3

## RESULT 12

US-10-709-691B-145999/c  
; Sequence 145999, Application US/10709691B  
; Publication No. US20070031843A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; APPLICANT: Bentwich, Itzhak  
; APPLICANT: Avniel, Amir

; TITLE OF INVENTION: Bioinformatically Detectable Group of Novel Regulatory Bacterial  
; FILE REFERENCE: Efs23  
; CURRENT APPLICATION NUMBER: US/10709,691B  
; CURRENT FILING DATE: 2004-05-24  
; NUMBER OF SEQ ID NOS: 4254815  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 145999  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human

US-10-709-691B-145999

Query Match 58.3%; Score 14; DB 9; Length 22;  
Best Local Similarity 78.6%; Pred. No. 1.8e+04;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGGGCGUGUUAAG 18  
|||||:|:|:|  
Db 16 AGGGGCTGGTTAAG 3

## RESULT 13

US-10-709-691B-153005/c  
; Sequence 153005, Application US/10709691B  
; Publication No. US20070031843A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; APPLICANT: Bentwich, Itzhak  
; APPLICANT: Avniel, Amir

; TITLE OF INVENTION: Bioinformatically Detectable Group of Novel Regulatory Bacterial  
; FILE REFERENCE: Efs23  
; CURRENT APPLICATION NUMBER: US/10709,691B  
; CURRENT FILING DATE: 2004-05-24  
; NUMBER OF SEQ ID NOS: 4254815  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 153005  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human

US-10-709-691B-153005

Query Match 58.3%; Score 14; DB 9; Length 22;  
Best Local Similarity 78.6%; Pred. No. 1.8e+04;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGGGCGUGUUAAG 18  
|||||:|:|:|  
Db 16 AGGGGCTGGTTAAG 3

## RESULT 14

US-10-709-691B-187400/c  
; Sequence 187400, Application US/10709691B  
; Publication No. US20070031843A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; APPLICANT: Bentwich, Itzhak  
; APPLICANT: Avniel, Amir

; TITLE OF INVENTION: Bioinformatically Detectable Group of Novel Regulatory Bacterial  
; FILE REFERENCE: Efs23  
; CURRENT APPLICATION NUMBER: US/10709,691B  
; CURRENT FILING DATE: 2004-05-24  
; NUMBER OF SEQ ID NOS: 4254815  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 187400  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human

US-10-709-691B-187400

Query Match 58.3%; Score 14; DB 9; Length 22;  
Best Local Similarity 78.6%; Pred. No. 1.8e+04;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGGGCGUGUUAAG 18  
|||||:|:|:|  
Db 16 AGGGGCTGGTTAAG 3

## RESULT 15

US-10-709-691B-197873/c  
; Sequence 197873, Application US/10709691B  
; Publication No. US20070031843A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; APPLICANT: Bentwich, Itzhak  
; APPLICANT: Avniel, Amir

; TITLE OF INVENTION: Bioinformatically Detectable Group of Novel Regulatory Bacterial  
; FILE REFERENCE: Efs23  
; CURRENT APPLICATION NUMBER: US/10709,691B  
; CURRENT FILING DATE: 2004-05-24  
; NUMBER OF SEQ ID NOS: 4254815  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 197873  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human

US-10-709-691B-197873

Query Match 58.3%; Score 14; DB 9; Length 22;  
Best Local Similarity 78.6%; Pred. No. 1.8e+04;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGGGCGUGUUAAG 18  
|||||:|:~|:|:|  
Db 16 AGGGGCTGGTTAAG 3

Search completed: June 19, 2007, 13:30:34  
Job time : 612.5 secs



GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 12:49:12 ; Search time 6876 Seconds  
(without alignments)  
216.548 Million cell updates/sec

Title: US-10-604-726a-6034

Perfect score: 24  
Sequence: 1 uagaggggucgguuagggcucc 24

Scoring table:  
IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 35954

Minimum DB seq length: 0  
Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST.\*  
1: gb\_est1.\*  
2: gb\_est3.\*  
3: gb\_est4.\*  
4: gb\_est5.\*  
5: gb\_est6.\*  
6: gb\_est7.\*  
7: gb\_est8.\*  
8: gb\_est9.\*  
9: gb\_est10.\*  
10: gb\_est11.\*  
11: gb\_est12.\*  
12: gb\_est13.\*  
13: gb\_est14.\*  
14: gb\_est15.\*  
15: gb\_est16.\*  
16: gb\_est17.\*  
17: gb\_est18.\*  
18: gb\_est19.\*  
19: gb\_est20.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12.6	52.5	24	15	AZ806300 2M0068F13
2	12	50.0	22	1	A1473941 tm04c11.x
3	12	50.0	25	11	R89803 YP91b12.r1
4	11.6	48.3	21	15	AZ654730
5	11.4	47.5	25	15	AZ794596
6	11.2	46.7	24	15	AZ341038
7	11.2	46.7	25	15	AZ820085
8	11	45.8	20	15	AZ846437
9	11	45.8	21	15	AZ493166
10	11	45.8	21	15	AZ836049
11	11	45.8	23	15	AZ945526
12	10.8	45.0	22	1	A1183338
13	10.6	44.2	20	15	AZ346729
14	10.6	44.2	25	15	AZ851549

C 15	10.4	43.3	19	15	AZ595016
C 16	10.4	43.3	22	1	AA978171
C 17	10.4	43.3	24	15	AZ786207
C 18	10.2	42.5	19	15	AZ331326
C 19	10.2	42.5	19	15	AZ345449
C 20	10.2	42.5	19	15	AZ345511
C 21	10.2	42.5	19	15	AZ345536
C 22	10.2	42.5	19	15	AZ345572
C 23	10.2	42.5	19	15	AZ346709
C 24	10.2	42.5	19	15	AZ346710
C 25	10.2	42.5	19	15	AZ368837
C 26	10.2	42.5	19	15	AZ447223
C 27	10.2	42.5	19	15	AZ447247
C 28	10.2	42.5	19	15	AZ510096
C 29	10.2	42.5	19	15	AZ510106
C 30	10.2	42.5	19	15	AZ638980
C 31	10.2	42.5	21	15	AZ495585
C 32	10.2	42.5	21	15	AZ510134
C 33	10.2	42.5	21	15	AZ645749
C 34	10.2	42.5	21	15	AZ850337
C 35	10.2	42.5	22	15	AZ785081
C 36	10	41.7	19	5	CA794263
C 37	10	41.7	20	15	AZ417235
C 38	10	41.7	22	15	AZ318425
C 39	10	41.7	22	15	AZ330040
C 40	10	41.7	22	15	AZ805739
C 41	10	41.7	23	7	AW246048
C 42	10	41.7	23	15	AZ989287
C 43	10	41.7	23	16	BH792606
C 44	10	41.7	25	15	AZ611099
C 45	10	41.7	25	15	AZ772979

#### ALIGNMENTS

RESULT 1  
AZ806300  
LOCUS  
DEFINITION  
2M0068F13F Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
clone UUGC2M0068F13 F, genomic survey sequence.  
ACCESSION  
AZ806300  
VERSION  
AZ806300.1 GI:12967111  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 24)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
JOURNAL  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112 USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0068 row: F column: 13  
Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 24.  
Location/Qualifiers  
1. .24  
/organism="Mus musculus"

/mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUC2M0068F13"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 52.5%; Score 12.6; DB 15; Length 24;  
 Best Local Similarity 57.9%; Pred. No. 7.7e+05;  
 Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 UCAGAGGGCGUGUUAAGG 19  
 :|||||:|:|:|:|:|:|  
 Db 5 TGGAGTGGGTGGTTAGGG 23

## RESULT 2

AI473941/c  
 LOCUS AI473941 22 bp mRNA linear EST 09-MAR-1999  
 DEFINITION tm04c11.x1 NCI CGAP Co14 Homo sapiens cDNA clone IMAGE:2155604 3'  
 similar to TR:Q06459 Q06459 NUCLEOLIN. 1, mRNA sequence.

ACCESSION AI473941  
 VERSION AI473941.1 GI:4326986  
 KEYWORDS EST.

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
 Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 22)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Tumor Gene Index  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

## JOURNAL

Unpublished (1997)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Greg Lennon, Ph.D.  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

## FEATURES

## source

1..22  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"

/db\_xref="taxon:9606"  
 /clone="IMAGE:2155604"  
 /tissue\_type="moderately-differentiated adenocarcinoma"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Co14"  
 /note="Organ: colon; Vector: pCMV-SPORT6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.7 kb. Life Technologies catalog #: 11531-019"

## ORIGIN

Query Match 50.0%; Score 12; DB 1; Length 22;  
 Best Local Similarity 70.0%; Pred. No. 1.4e+06;  
 Matches 14; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CAGAGGGCGUGUUAAGCG 21  
 |||||:|:|:|:|:|  
 Db 20 CAGAGGGCGAGGTCGAGGG 1

## RESULT 3

R89803/c  
 LOCUS R89803 25 bp mRNA linear EST 24-AUG-1995  
 DEFINITION YP91b12.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone  
 IMAGE:194783 5' similar to gb.X63526 ELONGATION FACTOR 1-GAMMA  
 (HUMAN); mRNA sequence.

ACCESSION R89803

VERSION R89803.1 GI:954630

KEYWORDS EST.

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
 Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 25)

## AUTHORS

Hillier, L., Clark, N., Dubucque, T., Elliston, K., Hawkins, M.,  
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
 Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
 Wilson, R.

The WashU-Merck EST Project

## JOURNAL

Unpublished (1995)

## COMMENT

Contact: Wilton RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 1193

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 1193 Std Error: 0.00

Seq primer: M13RP1

High quality sequence stop: 1.

## FEATURES

## source

1..25  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:3763833"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:194783"  
 /sex="male"

/dev\_stage="20 week-post conception fetus"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares fetal liver spleen INFLS"

/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)

with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;

1st strand cDNA was primed with a Pac I - oligo(dt) primer

[5' AACGGAAGAAATTAATAAGATCTTTTTTTTTTTTTTTT 3']

double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pTV73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 50.0%; Score 12; DB 11; Length 25;  
Best Local Similarity 75.0%; Pred. No. 1.4e+06;  
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGGGCGUGUUA 17  
|||||:|:|:|  
Db 12 GGGCGTGGTAA 1

RESULT 4

AZ654730/C 21 bp DNA linear GSS 14-DEC-2000

LOCUS IM0529P05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

DEFINITION clone UUGC1M0529P05 F, genomic survey sequence.

ACCESSION AZ654730

VERSION AZ654730.1 GI:11791876

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. 1 (bases 1 to 21)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0529 row: P column: 05  
Seq primer: CGTTGTAACGACGCCACT  
Class: plasmid ends  
High quality sequence stop: 21.

FEATURES

source

1..21

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0529P05"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 48.3%; Score 11.6; DB 15; Length 21;  
Best Local Similarity 66.7%; Pred. NO. 2.1e+06;  
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GAGAGGGCGUGUUAAG 19  
|||||:|:|:|  
Db 19 GGGTGGGATGGGTAAG 2

RESULT 5

AZ794596 25 bp DNA linear GSS 16-FEB-2001

LOCUS 2M0048M20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

DEFINITION clone UUGC2M0048M20 F, genomic survey sequence.

ACCESSION AZ794596

VERSION AZ794596.1 GI:12940723

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. 1 (bases 1 to 25)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0048 row: M column: 20  
Seq primer: CGTTGTAACGACGCCACT  
Class: plasmid ends  
High quality sequence stop: 25.

FEATURES

source

1..25

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0048M20"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 47.5%; Score 11.4; DB 15; Length 25;  
Best Local Similarity 57.1%; Pred. No. 2.6e+06;  
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 UGAGAGCGGCGUUAAGGCG 21  
: ||||| : : : : :  
DB 5 TGGAGGGGGGTGTGAGGGG 25

## RESULT 6

AZ341038/c 24 bp DNA linear GSS 29-SEP-2000  
LOCUS  
DEFINITION IM0073B16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0073B16 F, genomic survey sequence.

ACCESSION AZ341038.1 GI:10416890

VERSION

KEYWORDS

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidae; Muridae; Murinae; Mus.

## REFERENCE

## AUTHORS

1 (bases 1 to 24)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

## TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

## JOURNAL

## COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0073 row: B column: 16

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 24.

Location/Qualifiers

## FEATURES

## source

1..24  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0073B16"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

## ORIGIN

Query Match 46.7%; Score 11.2; DB 15; Length 24;  
Best Local Similarity 69.8%; Pred. No. 3.2e+06;  
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 GGGCGUGGUUAAGGCG 21  
||| : || : ||| :  
DB 18 GGGATGGGTAAAGTG 3

## RESULT 7

## LOCUS

AZ820085/c 25 bp DNA linear GSS 20-FEB-2001  
DEFINITION 2M0092001F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0092001 F, genomic survey sequence.

ACCESSION AZ820085

VERSION AZ820085.1 GI:12989993

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidae; Muridae; Murinae; Mus.

## REFERENCE

## AUTHORS

1 (bases 1 to 25)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

## TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

## JOURNAL

## COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0092 row: O column: 01

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 25.

Location/Qualifiers

## FEATURES

## source

1..25  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0092001"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to

electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 46.7%; Score 11.2; DB 15; Length 25;  
Best Local Similarity 68.8%; Pred. No. 3.2e+06;  
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 6 GGGGCGUGGUUAGGCG 21  
|||||:|||||:  
Db 19 GGGGATGGTAAAGTG 4

RESULT 8  
AZ846437  
LOCUS  
DEFINITION 2M0146E10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0146E10 R, genomic survey sequence.

ACCESSION  
AZ846437  
VERSION  
KEYWORDS  
SOURCE  
GSS.  
Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

## TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

## JOURNAL

## COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0146 row: E column: 10

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

## FEATURES

## source

1. -20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0146E10"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent *E. coli* XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## ORIGIN

Query Match 45.8%; Score 11; DB 15; Length 20;  
Best Local Similarity 57.9%; Pred. No. 3.9e+06;  
Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 UGAGAGGGCGUGGUUAGG 19  
:|||||:|||||:  
Db 2 TGGGATGGTGGTAGGG 20

## RESULT 9

## AZ493166

## LOCUS

DEFINITION 1M0327K05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0327K05 R, genomic survey sequence.

## ACCESSION

## AZ493166

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

## AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

## TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

## JOURNAL

## COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0327 row: K column: 05

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

## FEATURES

## source

1. -21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0327K05"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 45.8%; Score 11; DB 15; Length 21;  
Best Local Similarity 57.9%; Pred. No. 3.9e+06;  
Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 UGAGGGGCGUGGUUAGG 19  
:|||||||:|:|:|  
Db 2 TGGGAGTGGATGGGTAGG 20

## RESULT 10

AZ836049/c 21 bp DNA linear GSS 20-FEB-2001  
LOCUS  
DEFINITION 2M0130E11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0130E11 R, genomic survey sequence.

ACCESSION AZ836049  
VERSION 1  
KEYWORDS GI:13005957  
SOURCE GSS.

ORGANISM Mus musculus (house mouse)

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0130 row: E column: 11  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends

High quality sequence stop: 21.

## FEATURES

source

1..21  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0130E11"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 45.8%; Score 11; DB 15; Length 21;  
Best Local Similarity 90.9%; Pred. No. 3.9e+06;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AGAGGGGCGUG 13  
:|||||||:|:|:|  
Db 15 AGAGGGGCGTGG 5

## RESULT 11

AZ945526 25 bp DNA linear GSS 26-APR-2001  
LOCUS  
DEFINITION 2M0205L22R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0205L22 R, genomic survey sequence.

ACCESSION AZ945526  
VERSION 1  
KEYWORDS GI:13809815  
SOURCE GSS.

ORGANISM Mus musculus (house mouse)

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 25)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0206 row: L column: 22  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends

High quality sequence stop: 25.

## FEATURES

source

1..25  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0205L22"  
/sex="Female"

/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWP42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 45.8%; Score 11; DB 15; Length 25;  
Best Local Similarity 57.9%; Pred. No. 4e+06;  
Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 UGAGAGGGGCGUGUUAAGG 19  
: ||||| : : : : :  
Db 5 TGGGAGTGGGTGGGTAGCG 23

## RESULT 12

Al183338/c

## LOCUS

DEFINITION qd41a12.x1 Soares fetal heart NBHH19W Homo sapiens cDNA clone IMAGE:1732030 3' similar to TR:Q18444 Q18444 COSMID C34D4. ;, mRNA sequence.

## ACCESSION

Al183338 1 GI:3733976

## VERSION

Al183338

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;

Catarrhini; Homidae; Homo.

1 (bases 1 to 22)

NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: [cgaps-rc@mail.nih.gov](mailto:cgaps-rc@mail.nih.gov)

This clone is available royalty-free through LNL; contact the

IMAGE Consortium ([info@image.llnl.gov](http://info.image.llnl.gov)) for further information.

Trace considered overall poor quality

Insert Length: 698 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1. .22

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1732030"

/sex="unknown"

/dev\_stage="19 weeks"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares fetal heart NBHH19W"

/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a

modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAATGAGCGCGCATCTTTTTTTTTTTT 3']

double-stranded cDNA was size selected, ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT7T3 vector

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by

M.Fatima Bonaldo. This library was constructed from the

same fetus as the fetal lung library, Soares fetal lung

## ORIGIN

Query Match 45.0%; Score 10.8; DB 1; Length 22;  
Best Local Similarity 64.3%; Pred. No. 4.9e+06;  
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAGAGGGGCGUGUU 15  
: ||||| : : : : :  
Db 17 GAGTGGGGGTGGTT 4

## RESULT 13

AZ346729/c

## LOCUS

DEFINITION IM0082A10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0082A10 F, genomic survey sequence.

## ACCESSION

AZ346729

## VERSION

AZ346729.1 GI:10425966

## KEYWORDS

GSS.

## SOURCE

Mus musculus (house mouse)

## ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridea; Murinae; Mus.

1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausen, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)

Insert Length: 10000 Std Error: 0.00

Plate: 0082 row: A column: 10

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1. .20

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0082A10"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWP42 [gi|4732114|gb|AF129072.1], a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells



and selected for ampicillin resistance."

# ORIGIN

Query Match 44.2%; Score 10.6; DB 15; Length 20;  
 Best Local Similarity 64.7%; Pred. No. 5.9e+06;  
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 GAGAGGGGCGUGUUAAG 18  
 |||||:||||  
 Db 20 GAGTGAGGTTGGTGAAG 4

# RESULT 14

AZ851549/c  
 LOCUS 25 bp DNA linear GSS 21-FEB-2001  
 DEFINITION 2M0153P13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0153P13 R, genomic survey sequence.  
 ACCESSION AZ851549  
 VERSION AZ851549.1 GI:13037657  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 25)

REFERENCE  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Kelly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

UNPUBLISHED (2000)

CONTACT: Robert B. Weiss  
 UNIVERSITY OF UTAH  
 RM. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0153 row: P column: 13  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: Plasmid ends  
 High quality sequence stop: 25.

# FEATURES

source

1..25  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0153P13"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

# ORIGIN

Query Match 44.2%; Score 10.6; DB 15; Length 25;  
 Best Local Similarity 64.7%; Pred. No. 6e+06;  
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 3 AGAGGGGCGUGUUAAGG 19  
 |||||:||||  
 Db 25 AGAGGGTAAAGGTTAAGG 9

# RESULT 15

AZ595016/c  
 LOCUS 19 bp DNA linear GSS 13-DEC-2000  
 DEFINITION 1M0407C19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0407C19 F, genomic survey sequence.

ACCESSION AZ595016

VERSION AZ595016.1

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 19)

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Kelly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

UNPUBLISHED (2000)

CONTACT: Robert B. Weiss

UNIVERSITY OF UTAH

RM. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0407 row: C column: 19  
 Seq primer: CGTTGTAAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence stop: 19.

# FEATURES

source

1..19  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0407C19"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to



adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## ORIGIN

Query Match 43.3%; Score 10.4; DB 15; Length 19;  
Best Local Similarity 75.0%; Pred. No. 7.3e+06;  
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 UGAGAGGGGCTG 12  
:|||||:  
Db 17 TGGAGGGGCTG 6

Search completed: June 19, 2007, 20:24:43  
Job time : 6878 secs